```
SIGNAL      1 atggatgtggcggccgctgcgttgcctgctttgtagctctctggcttctgtacccgtgg  60
PEPTIDE     1 [M D V A A A A L P A F V A L W L L Y P W                    20

           61 cctctcctgggglcggcccttggccagttctcagcagglggctgtactttgatgatggg 120
           21 P L L G S]A L G Q F S A[G G C T F D D G                    40

A5
HOMOLOGY   121 ccaggggcttgtgactaccaccaggatttatacgatgactttgagtgggtccatgtcagt 180
REGION      41 P G A C D Y H Q D L Y D D F E W V H V S                    60

           181 gcgcaggaacctcattacctgccccccgaaatgcctcaaggttcctatatggttgtggac 240
            61 A Q E P H Y L P P E M P Q G S Y M V V D                    80

           241 tcctcaaatcatgatcctggagaaaaagccagacttcagctgcctaccatgaaggagaat 300
            81 S S N H D P G E K A R L Q L P T M K E N                    100

           301 gacacccactgcattgatttcagttacctgttatatagccagaaggggttgaaccctggc 360
           101 D T H C I D F S Y L L Y S Q K G L N P G                    120

           361 actttgaatatcctagttagggtgaataaaggacctcttgctaatccaatttggaatgta 420
           121 T L N I L V R V N K G P L A N P I W N V                    140

           421 actggattcactggtcgtgattggcttcgggctgaactagctgtgagcacctttttggccc 480
           141 T G F T G R D W L R A E L A V S T F W P                    160

           481 aatgaataccaggtaatatttgaagctgaagtctcaggagggagaagtggttatattgcc 540
           161 N E Y Q V I F E A E V S G G R S G Y I A                    180

           541 attgatgacatccaagtcctgagttatccttgcgataaatctcctcatttttctccgcctt 600
           181 I D D I Q V L S Y]P C D K S P H F L R L                    200
```

FIG.1A

```
601  ggtgatgtggaggtcaatgctgggcagaatgctacatttcagtgcattgctacagggaga  660
201  G  D  V  E  V  N  A  G  Q  N  A  T  F  Q  C  I  A  T  G  R   220

661  gatgctgtgcataacaagttatggctgcagagacgcaatggagaagacatacccgtagcc  720
221  D  A  V  H  N  K  L  W  L  Q  R  R  N  G  E  D  I  P  V  A   240

721  cagactaagaacataaatcacagaagatttgctgcctctttcagattgcaagaagtgaca  780
241  Q  T  K  N  I  N  H  R  R  F  A  A  S  F  R  L  Q  E  V  T   260

781  aaaactgaccaggatttgtaccgctgcgtaactcagtcagaacgaggttctggggtttcc  840
261  K  T  D  Q  D  L  Y  R  C  V  T  Q  S  E  R  G  S  G  V  S   280

841  aattttgctcaactcattgtgagagaaccacctagacccattgctcctccccagctgctt  900
281  N  F  A  Q  L  I  V  R  E  P  P  R  P  I  A  P  P  Q  L  L   300

901  ggtgttgggcctacttacttgctgatccaactaaatgccaactctattattggcgatggc  960
301  G  V  G  P  T  Y  L  L  I  Q  L  N  A  N  S  I  I  G  D  G   320

961  cccatcatcctgaaagaagtagagtatcgaatgacatcaggatcttggacagaaacccat 1020
321  P  I  I  L  K  E  V  E  Y  R  M  T  S  G  S  W  T  E  T  H   340

1021 gcagtcaacgcaccaacatataagttgtggcatttagacccagatacagaatacgagatc 1080
341  A  V  N  A  P  T  Y  K  L  W  H  L  D  P  D  T  E  Y  E  I   360

1081 cgcgtcctgcttaccagacctggcgaaggggggaactgggctgccaggaccaccactgatc 1140
361  R  V  L  L  T  R  P  G  E  G  G  T  G  L  P  G  P  P  L  I   380

1141 actagaacgaagtgtgcagaacctatgcggacaccaaagactttaaagattgctgaaatc 1200
381  T  R  T  K  C  A  E  P  M  R  T  P  K  T  L  K  I  A  E  I   400
```

FIG.1B

```
1201  caggcaaggcgcattgcagtggactgggagtccttgggctacaacatcactcgttgccac  1260
 401  Q  A  R  R  I  A  V  D  W  E  S  L  G  Y  N  I  T  R  C  H   420

1261  actttcaacgtcactatctgctaccattacttccgtggccacaatgagagcagggcagac  1320
 421  T  F  N  V  T  I  C  Y  H  Y  F  R  G  H  N  E  S  R  A  D   440

1321  tgcttggacatggaccccaaagcccctcagcatgttgtgaaccatctgccaccttacaca  1380
 441  C  L  D  M  D  P  K  A  P  Q  H  V  V  N  H  L  P  P  Y  T   460

1381  aatgtcagcctcaagatgatcctaaccaacccagagggaaggaaggagagcgaagagaca  1440
 461  N  V  S  L  K  M  I  L  T  N  P  E  G  R  K  E  S  E  E  T   480

1441  atcatccaaactgatgaagatgtgcccgggcctgtgccagtcaaatccctccaaggaaca  1500
 481  I  I  Q  T  D  E  D  V  P  G  P  V  P  V  K  S  L  Q  G  T   500

1501  tcctttgaaaacaagatcttcctgaactggaaagagccactggaaccgaatggaattatc  1560
 501  S  F  E  N  K  I  F  L  N  W  K  E  P  L  E  P  N  G  I  I   520

1561  actcagtatgaggtgagctatagcagcataagatcatttgaccctgctgttccagtggct  1620
 521  T  Q  Y  E  V  S  Y  S  S  I  R  S  F  D  P  A  V  P  V  A   540

1621  gggccccccacagactgtatcaaatttatggaatagtacacaccatgtatttatgcatctt  1680
 541  G  P  P  Q  T  V  S  N  L  W  N  S  T  H  H  V  F  M  H  L   560

1681  caccctggaaccacctaccagttttttataagagccagcactgtcaaaggctttggacca  1740
 561  H  P  G  T  T  Y  Q  F  F  I  R  A  S  T  V  K  G  F  G  P   580

1741  gcaacagccatcaatgtgaccacaaatatctcagctccaagcttacctgactatgaagga  1800
 581  A  T  A  I  N  V  T  T  N  I  S  A  P  S  L  P  D  Y  E  G   600
```

FIG.1C

```
1801  gttgatgcctctctgaatgaaactgccaccaccatcacagtactattgaggcctgcacaa  1860
 601  V  D  A  S  L  N  E  T  A  T  T  I  T  V  L  L  R  P  A  Q    620

1861  gccaaaggtgctcctatcagtgcttatcaaattgttgtggagcagctacacccacatcga  1920
 621  A  K  G  A  P  I  S  A  Y  Q  I  V  V  E  Q  L  H  P  H  R    640

1921  acgaagcgtgaagcaggggccatggaatgctaccaggtaccggttacataccagaacgcc  1980
 641  T  K  R  E  A  G  A  M  E  C  Y  Q  V  P  V  T  Y  Q  N  A    660

1981  ctaagtgggggcgcgccctattacttgccgcagaacttcccctgggaatcttcccgag    2040
 661  L  S  G  G  A  P  Y  Y  F  A  A  E  L  P  P  G  N  L  P  E    680

2041  cctgctccctttcaccgtgggtgacaaccggacctataaaggctttggaacccttccctg  2100
 681  P  A  P  F  T  V  G  D  N  R  T  Y  K  G  F  W  N  P  P  L    700

2101  gcccccgcaaaggatacaacatctatttccaagcgatgagcagtgtggagaaggaaact   2160
 701  A  P  R  K  G  Y  N  I  Y  F  Q  A  M  S  S  V  E  K  E  T    720

2161  aaaacccaatgtgtacgaattgctacaaaagcagcagcaacagaagaaccagaagtgatc  2220
 721  K  T  Q  C  V  R  I  A  T  K  A  A  A  T  E  E  P  E  V  I    740

2221  ccagacccggcaaagcagacagacagagtggtgaagatcgcgggcatcagtgctggcatc  2280
 741  P  D  P  A  K  Q  T  D  R  V  V  K [I  A  G  I  S  A  G  I    760
TRANS-
MEMBRANE

2281  ctagtgttcatccttctcctgctggttgtcatagtaattgtgaaaaagagcaagcttgct  2340
 761  L  V  F  I  L  L  L  L  V  V  I  V  I  V] K  K  S  K  L  A    780

2341  aagaagcgcaaagatgcaatggggaacacacgtcaggagatgacccacatggtgaatgct  2400
 781  K  K  R  K  D  A  M  G  N  T  R  Q  E  M  T  H  M  V  N  A    800
```

FIG.1D

```
          2401  atggaccgaagttatgctgaccagagcaccctgcatgcagaagacccccttttccctcacc  2460
           801  M  D  R  S  Y  A  D  Q  S  T  L  H  A  E  D  P  L  S  L  T    820

          2461  ttcatggaccaacataacttcagtccaagattgcccaatgatccacttgtgccgactgcc  2520
           821  F  M  D  Q  H  N  F  S  P  R  L  P  N  D  P  L  V  P  T  A    840

          2521  gtgttagatgagaaccacagtgccacagcagagtctagtcgtctcctggatgttcctcga  2580
           841  V  L  D  E  N  H  S  A  T  A  E  S  S  R  L  L  D  V  P  R    860

          2581  tacctctgcgaagggacagagtcccctiatcagacaggacagctgcacccagccatcagg  2640
           861  Y  L  C  E  G  T  E  S  P  Y  Q  T  G  Q  L  H  P  A  I  R    880

          2641  gtggccgacttactgcagcacattaacctcatgaagacatcagacagctatgggttcaaa  2700
           881  V  A  D  L  L  Q  H  I  N  L  M  K  T  S  D  S  Y  G  F  K    900

          2701  gaggaatacgagagcttctttgaaggccagtcagcctctgggatgtggctaaaaaggat  2760
           901  E  E  Y  E  S  F  F  E  G  Q  S  A  S  W  D  V  A  K  K  D    920

PTPase    2761  caaaacagagcaaagaaccgatacggaaacattatcgcatatgatcactccagagtcatc  2820
DOMAIN I   921  Q  N  R  A  K [N  R  Y  G  N  I  I  A  Y  D  H  S  R  V  I    940

          2821  ctgcaacctgtggaagatgacccttcttcagattacattaatgccaactacatcgacatt  2880
           941  L  Q  P  V  E  D  D  P  S  S  D  Y  I  N  A  N  Y  I  D  I    960

          2881  tggctgtacagggatggctaccagagccaagccactacattgcaactcaaggcccagtt  2940
           961  W  L  Y  R  D  G  Y  Q  R  P  S  H  Y  I  A  T  Q  G  P  V    980

          2941  catgaaaccgtatatgattttttggaggatggtgtggcaagagcagtctgcctgtattgtg  3000
           981  H  E  T  V  Y  D  F  W  R  M  V  W  Q  E  Q  S  A  C  I  V   1000
```

FIG.1E

```
3001  atggtcactaatttagtggaagttggccgggtgaaatgctataaatattggcctgatgat  3060
1001  M  V  T  N  L  V  E  V  G  R  V  K  C  Y  K  Y  W  P  D  D    1020

3061  actgaggtttatggtgacttcaaagtcacctgcgtagaaatggagccacttgctgagtat  3120
1021  T  E  V  Y  G  D  F  K  V  T  C  V  E  M  E  P  L  A  E  Y    1040

3121  gtcgttaggacattcaccttggaaaggaggggctataatgaaatccgtgaagtcaaacag  3180
1041  V  V  R  T  F  T  L  E  R  R  G  Y  N  E  I  R  E  V  K  Q    1060

3181  ttccacttcactggctggcctgaccatggtgttccataccacgcaacagggctcctgtca  3240
1061  F  H  F  T  G  W  P  D  H  G  V  P  Y  H  A  T  G  L  L  S    1080

3241  tttatccggagagtcaagctatctaaccctcccagtgctgggcccattgtcgtacactgc  3300
1081  F  I  R  R  V  K  L  S  N  P  P  S  A  G  P  I  V  V  H  C    1100

3301  agtgctggtgctgggcgcacaggctgttacattgttattgacataatgctggacatggct  3360
1101  S  A  G  A  G  R  T  G  C  Y  I  V  I  D  I  M  L  D  M  A    1120

3361  gaaagagagggtgtggttgacatctacaactgtgtgaaagccttacgatctcggcgcatt  3420
1121  E  R  E  G  V  V  D  I  Y  N  C  V  K  A  L  R  S  R  R  I    1140

3421  aatatggtacagacagaggaacagtacatttttattcatgatgccatttagaagcctgc  3480
1141  N  M  V  Q  T  E  E  Q  Y  I  F  I  H  D  A  I  L  E] A  C    1160

3481  ttatgtggagaaactgccatccctgtgtgtgaatttaaagctgcatattttgatatgatt  3540
1161  L  C  G  E  T  A  I  P  V  C  E  F  K  A  A  Y  F  D  M  I    1180

3541  cgaatagactctcagactaactcctctcatctcaaagatgaatttcagactctgaattcg  3540
1161  L  C  G  E  T  A  I  P  V  C  E  F  K  A  A  Y  F  D  M  I    1180
```

FIG.1F

```
                3541  cgaatagactctcagactaactcctctcatctcaaagatgaatttcagactctgaattcg  3600
                1181  R  I  D  S  Q  T  N  S  S  H  L  K  D  E  F  Q  T  L  N  S   1200

PTPase          3601  gtcacccctcgactacaagctgaagactgcagcatagcctgcctgccaaggaaccatgac  3660
DOMAIN II       1201  V  T  P  R  L  Q  A  E  D  C  S  I  A  C  L  P  R [N  H  D   1220

                3661  aagaaccgtttcatggatatgctcccacctgacagatgtctgccttttttaattacaatt  3720
                1221  K  N  R  F  M  D  M  L  P  P  D  R  C  L  P  F  L  I  T  I   1240

                3721  gatggggagagcagtaactacatcaatgctgctcttatggatagctatatggcagccagca  3780
                1241  D  G  E  S  S  N  Y  I  N  A  A  L  M  D  S  Y  R  Q  P  A   1260

                3781  gctttcatcgtcacacaatacccactgccaaacactgtgaaagacttctggagattagta  3840
                1261  A  F  I  V  T  Q  Y  P  L  P  N  T  V  K  D  F  W  R  L  V   1280

                3841  tatgattacggatgtacctccatcgtgatgctaaatgaagtggacctgtctcagggctgc  3900
                1281  Y  D  Y  G  C  T  S  I  V  M  L  N  E  V  D  L  S  Q  G  C   1300

                3901  ccacagtactggccagaagaaggaatgctgcgatatggtcctatccaagtggaatgtatg  3960
                1301  P  Q  Y  W  P  E  E  G  M  L  R  Y  G  P  I  Q  V  E  C  M   1320

                3961  tcttgttcaatggactgtgatgtgatcaatcgaatttttagaatatgcaacctaacgaga  4020
                1321  S  C  S  M  D  C  D  V  I  N  R  I  F  R  I  C  N  L  T  R   1340

                4021  ccacaggagggctatctgatggtacaacagttccagtacctaggctgggcttctcatcga  4080
                1341  P  Q  E  G  Y  L  M  V  Q  Q  F  Q  Y  L  G  W  A  S  H  R   1360

                4081  gaagtgcctggctccaaacgctcgttttgaaattgatactgcaggtggaaaaatggcaa  4140
                1361  E  V  P  G  S  K  R  S  F  L  K  L  I  L  Q  V  E  K  W  Q   1380
```

FIG.1G

```
4141  gaggaatgtgaagaaggggaaggccggacaatcatccactgcttgaatggcggtgggcgc  4200
1381  E  E  C  E  E  G  E  G  R  T  I  I  H  C  L  N  G  G  G  R    1400

4201  agtggcatgttctgtgccataggcattgttgtggagatggtgaagcggcaaaatgtggtg  4260
1401  S  G  M  F  C  A  I  G  I  V  V  E  M  V  K  R  Q  N  V  V    1420

4261  gatgttttccatgcagtaaagacgctgaggaacagcaagccaaacatggtggaagccccg  4320
1421  D  V  F  H  A  V  K  T  L  R  N  S  K  P  N  M  V  E  A  P    1440

4321  gagcagtatcgtttttgctatgatgtggcgttagagtacctgggagtcctcatag  4374
1441  E  Q  Y  R  F  C  Y  D  V  A  L  E  Y  L  E]S  S  *      1458
```

FIG. 1H

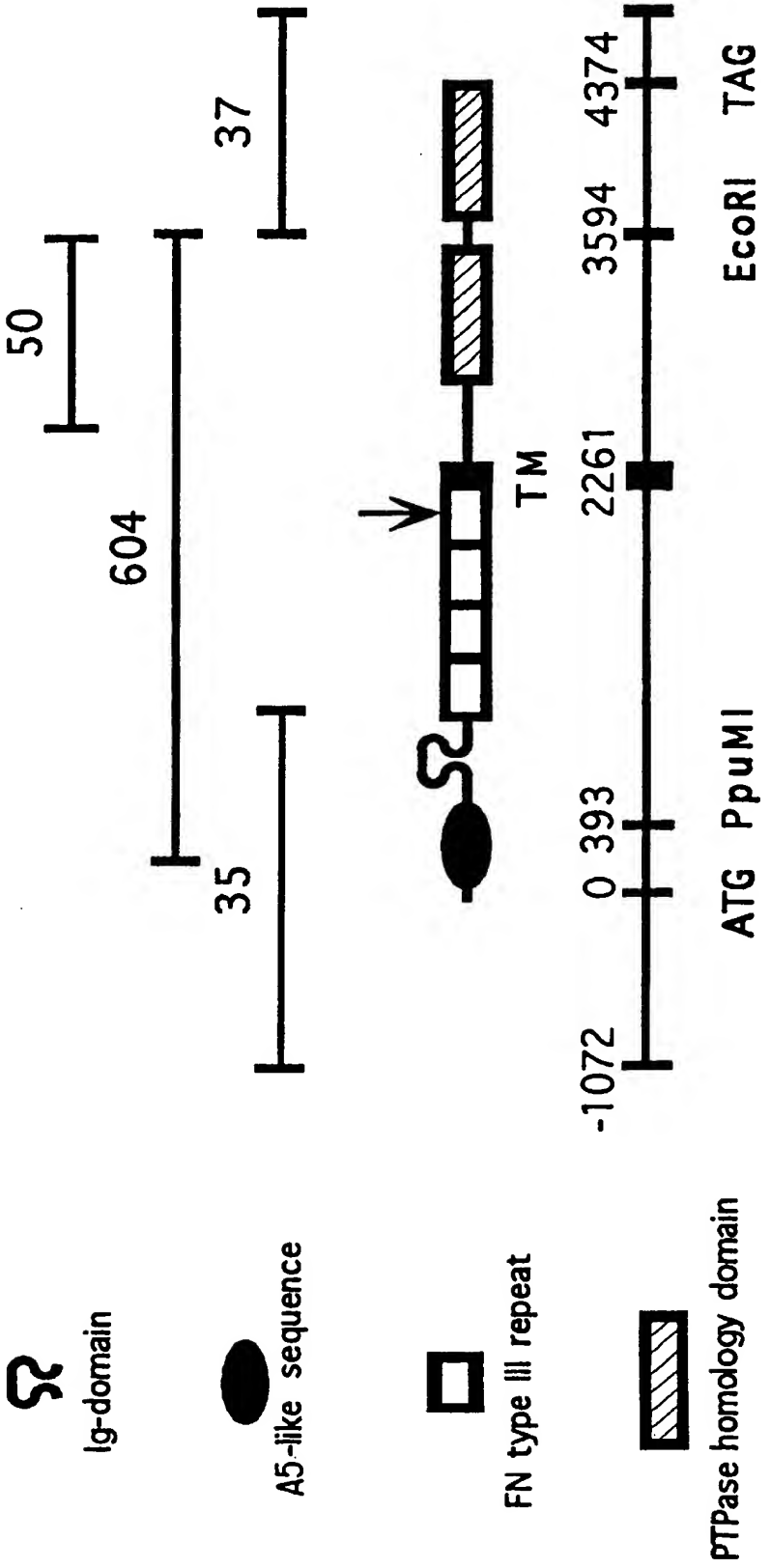

50
604
35
37
TM
-1072
0
393
2261
3594
4374
ATG
PpuMI
EcoRI
TAG
Ig-domain
A5-like sequence
FN type III repeat
PTPase homology domain

FIG. 2

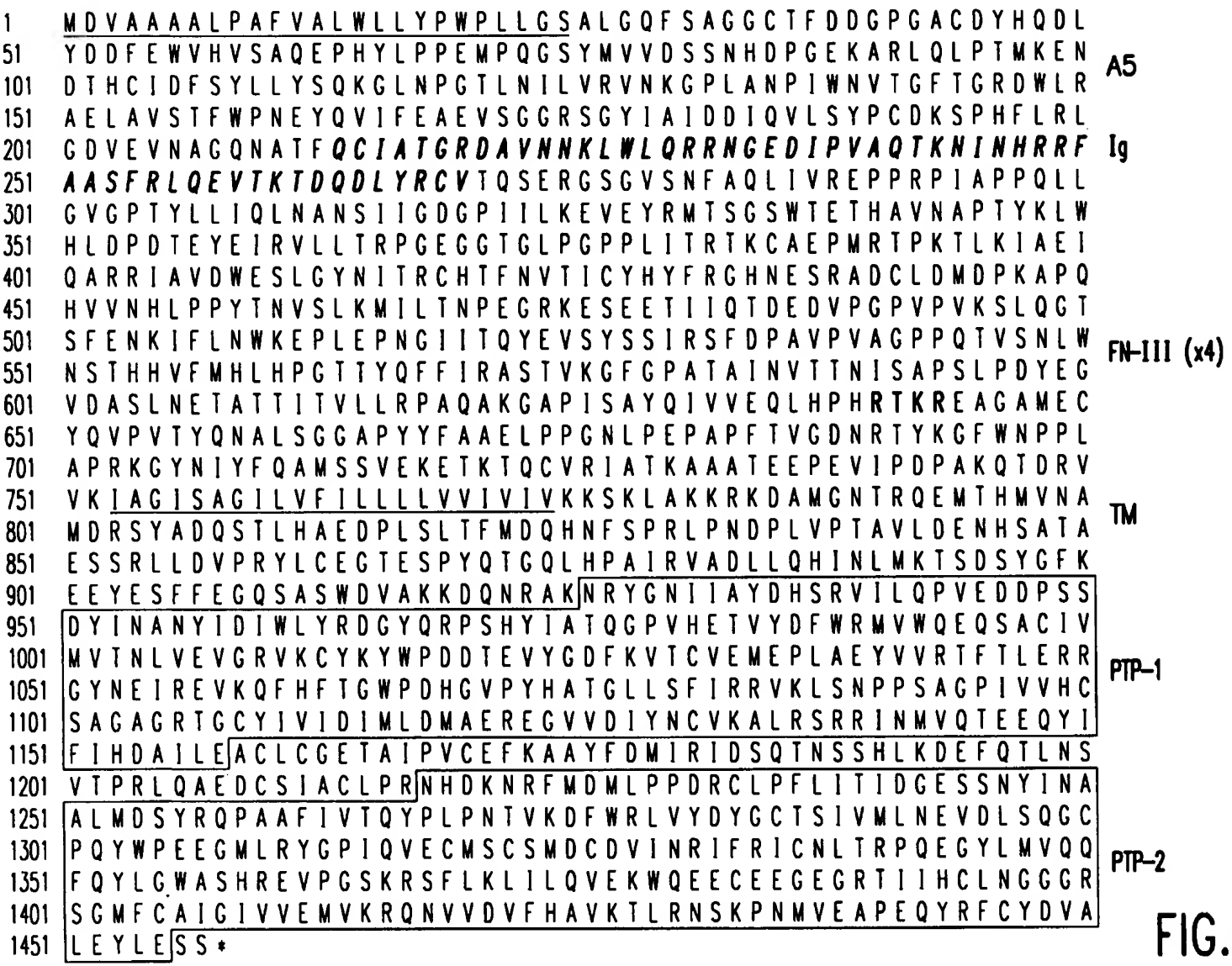

1 MDVAAAALPAFVALWLLYPWPLLGSALGQFSAGGCTFDDGPGACDYHQDL
51 YDDFEWVHVSAQEPHYLPPEMPQGSYMVVDSSNHDPGEKARLQLPTMKEN
101 DTHCIDFSYLLYSQKGLNPGTLNILVRVNKGPLANPIWNVTGFTGRDWLR
151 AELAVSTFWPNEYQVIFEAEVSGGRSGYIAIDDIQVLSYPCDKSPHFLRL
201 GDVEVNAGQNATFQCIATGRDAVNNKLWLQRRNGEDIPVAQTKNINHRRF
251 AASFRLQEVTKTDQDLYRCVTQSERGSGVSNFAQLIVREPPRPIAPPQLL
301 GVGPTYLLIQLNANSIIGDGPIILKEVEYRMTSGSWTETHAVNAPTYKLW
351 HLDPDTEYEIRVLLTRPGEGGTGLPGPPLITRTKCAEPMRTPKTLKIAEI
401 QARRIAVDWESLGYNITRCHTFNVTICYHYFRGHNESRADCLDMDPKAPQ
451 HVVNHLPPYTNVSLKMILTNPEGRKESEETIIQTDEDVPGPVPVKSLQGT
501 SFENKIFLNWKEPLEPNGIITQYEVSYSSIRSFDPAVPVAGPPQTVSNLW
551 NSTHHVFMHLHPGTTYQFFIRASTVKGFGPATAINVTTNISAPSLPDYEG
601 VDASLNETATTITVLLRPAQAKGAPISAYQIVVEQLHPHRTKREAGAMEC
651 YQVPVTYQNALSGGAPYYFAAELPPGNLPEPAPFTVGDNRTYKGFWNPPL
701 APRKGYNIYFQAMSSVEKETKTQCVRIATKAAATEEPEVIPDPAKQTDRV
751 VKIAGISAGILVFILLLLVVIVIVKKSKLAKKRKDAMGNTRQEMTHMVNA
801 MDRSYADQSTLHAEDPLSLTFMDQHNFSPRLPNDPLVPTAVLDENHSATA
851 ESSRLLDVPRYLCEGTESPYQTGQLHPAIRVADLLQHINLMKTSDSYGFK
901 EEYESFFEGQSASWDVAKKDQNRAKNRYGNIIAYDHSRVILQPVEDDPSS
951 DYINANYIDIWLYRDGYQRPSHYIATQGPVHETVYDFWRMVWQEQSACIV
1001 MVTNLVEVGRVKCYKYWPDDTEVYGDFKVTCVEMEPLAEYVVRTFTLERR
1051 GYNEIREVKQFHFTGWPDHGVPYHATGLLSFIRRVKLSNPPSAGPIVVHC
1101 SAGAGRTGCYIVIDIMLDMAERECVVDIYNCVKALRSRRINMVQTEEQYI
1151 FIHDAILEACLCGETAIPVCEFKAAYFDMIRIDSQTNSSHLKDEFQTLNS
1201 VTPRLQAEDCSIACLPRNHDKNRFMDMLPPDRCLPFLITIDGESSNYINA
1251 ALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIVMLNEVDLSQGC
1301 PQYWPEEGMLRYGPIQVECMSCSMDCDVINRIFRICNLTRPQEGYLMVQQ
1351 FQYLGWASHREVPGSKRSFLKLILQVEKWQEECEEGEGRTIIHCLNGGR
1401 SGMFCAIGIVVEMVKRQNVVDVFHAVKTLRNSKPNMVEAPEQYRFCYDVA
1451 LEYLESS*
A5
Ig
FN-III (x4)
TM
PTP-1
PTP-2

FIG.3

```
          *    *          *    *         *   *   *              *                    *   **    *       *
I (296)   P PQL L GVGPTYLLIQLNANS I IGDGPIILKEVE Y RMTSGSWTETHAVNAPTYKLWHLDPDTE.YEIRVLL T R PG EG G TGLPGPPLITRT
II (392)  P .KT L KIAEIQA..RRIAVD W ESLGYNITRCHT F NVTICYHYFRGHNESRADCLDMDPKA...PQHVVNH L P PY TN V SLKMIL.TNPEG
III (493) P VKS L QGTSFE...NKIFLN W KEPLEPNGIITQ Y EVSYSSIRSFDPAVPVAGPPQTVSNLWNSTHHVFMH L H PG TT Y QFFIRASTVKGF
IV (596)  P DYE G VDASLNETATTITVL L RPAQAKGAPISA Y QIVVEQLHPHRTKR.EAGAMECYQV....PVTYQNA L S GG AP Y YFAAELPPGNLP
FBN-III(7) P PTN L HLEANPDT.GVLTVS W ERSTTPD..ITG Y RITTTPTNGQQGNSLEEVVHADQ......SSCTFDN L S PG LE Y NVSVY..TVKDD
```

FIG.4

```
PTP-κ(34)    GGCTFDDGPGACDYHQDLYDDFEWVHVSAQE.PHYLPPEMPQGSYMVVDSSNHDPGEKARLQLPTMKEN.DTHCIDFSYLLYSQK
PTP-μ(26)    GGCLFDEPYSTCGYSQADEDDFNWEQVNTLTKPT.SDPWMPSGSFMLVNTSGKPEGQRAHLLLPQLKEN.DTHCIDFHYFVSSKS
A5  (651)    CKFGWGSQKTVCNWQHDISSDLKWAVLNSKTGP..VQDHTGDGNFIYSEADERHEGRAARLMSPVVSSSRSAHCLTFWYHM...D
Consensus    ----------C---D---D--W---N--T-P--------G-F--------EG--ARL--P--------HC--F-Y------

PTP- κ       GLNPGTLNILVRVN.KGPLANPIWNVTGFTGRDWLRAELAVSTFWPNEYQVIFEAEVSGGRSGYIAIDDIQVLSY
PTP- μ       NAAPGLLNVYVKVN.NGPLGNPIWNISGDPTRTWHRAELAISTFWPNFYQVIFEV.VTSGHQGYLAIDEVKVLGH
A5           GSHVGTLSIKLKYEMEEDFDQTLWTVSGNQGDQWKEARVVLHKTMKQ.YQVIVEGTVGKGSAGGIAVDDIIIANH
Consensus    G---GTL-I--K----------W-VSG--G--W--A----------YQVI-E--V--G--G-IA-DDI----H
```

FIG.5

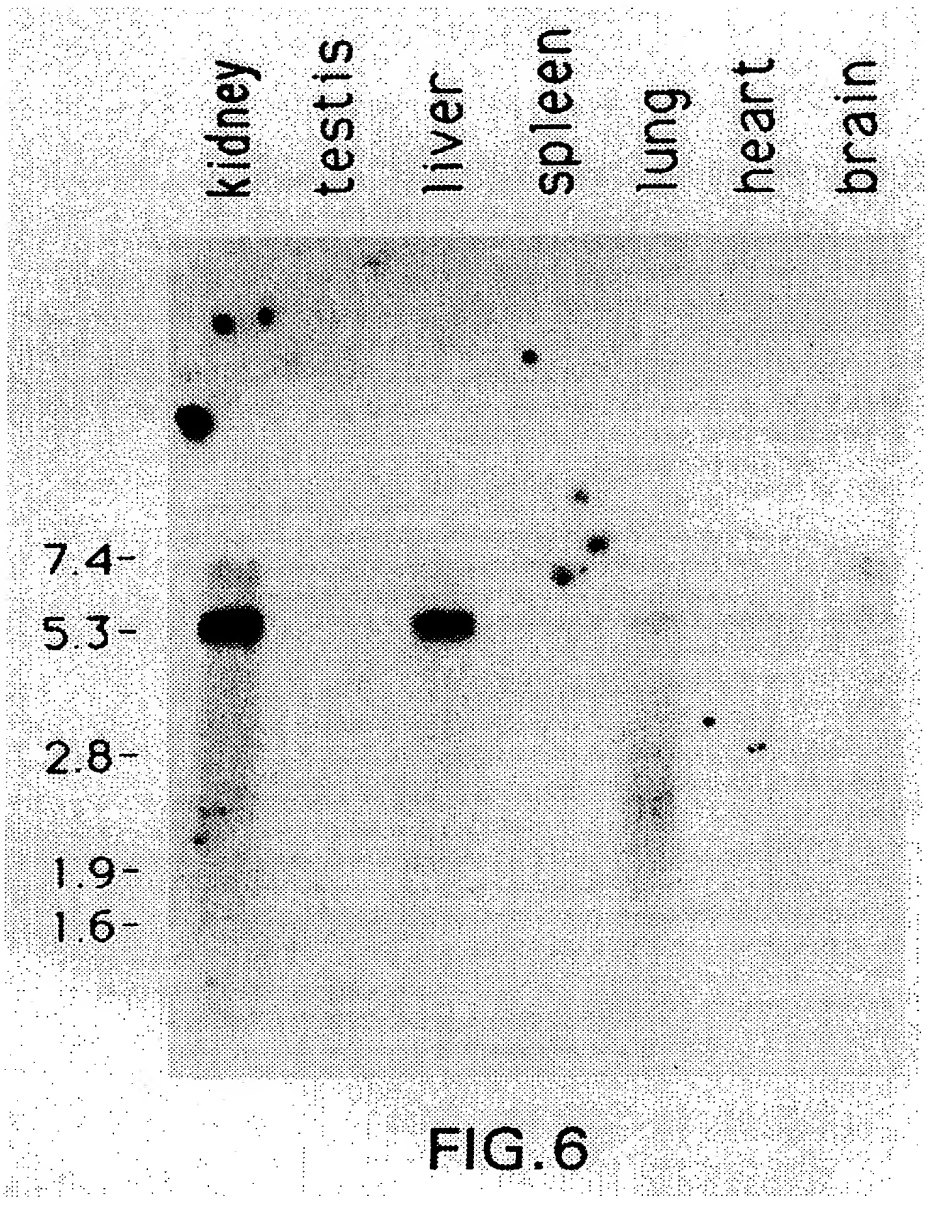


FIG.6

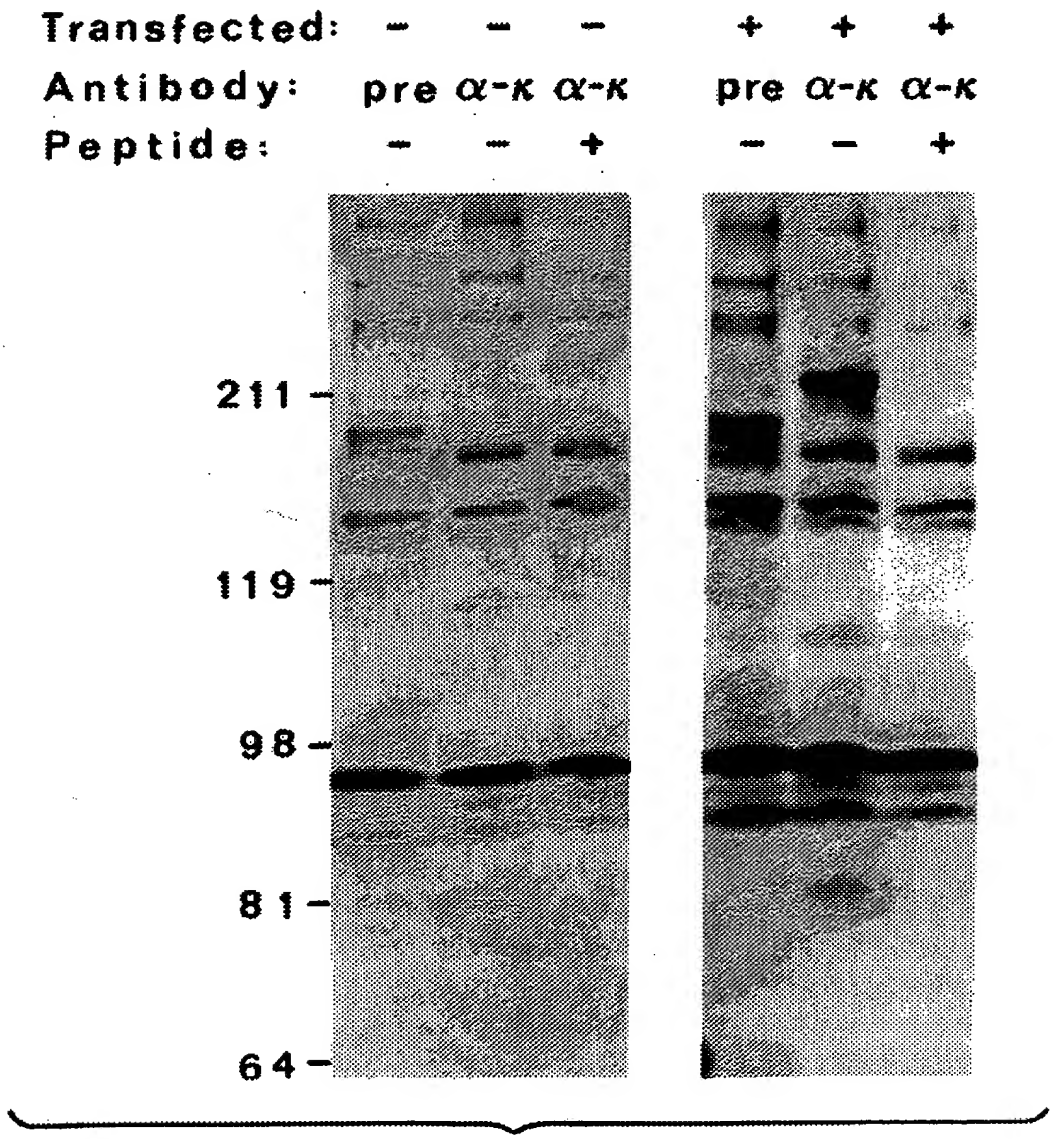

Transfected: - - - + + +
Antibody: pre α-κ α-κ pre α-κ α-κ
Peptide: - - + - - +
211
119
98
81
64

FIG. 7

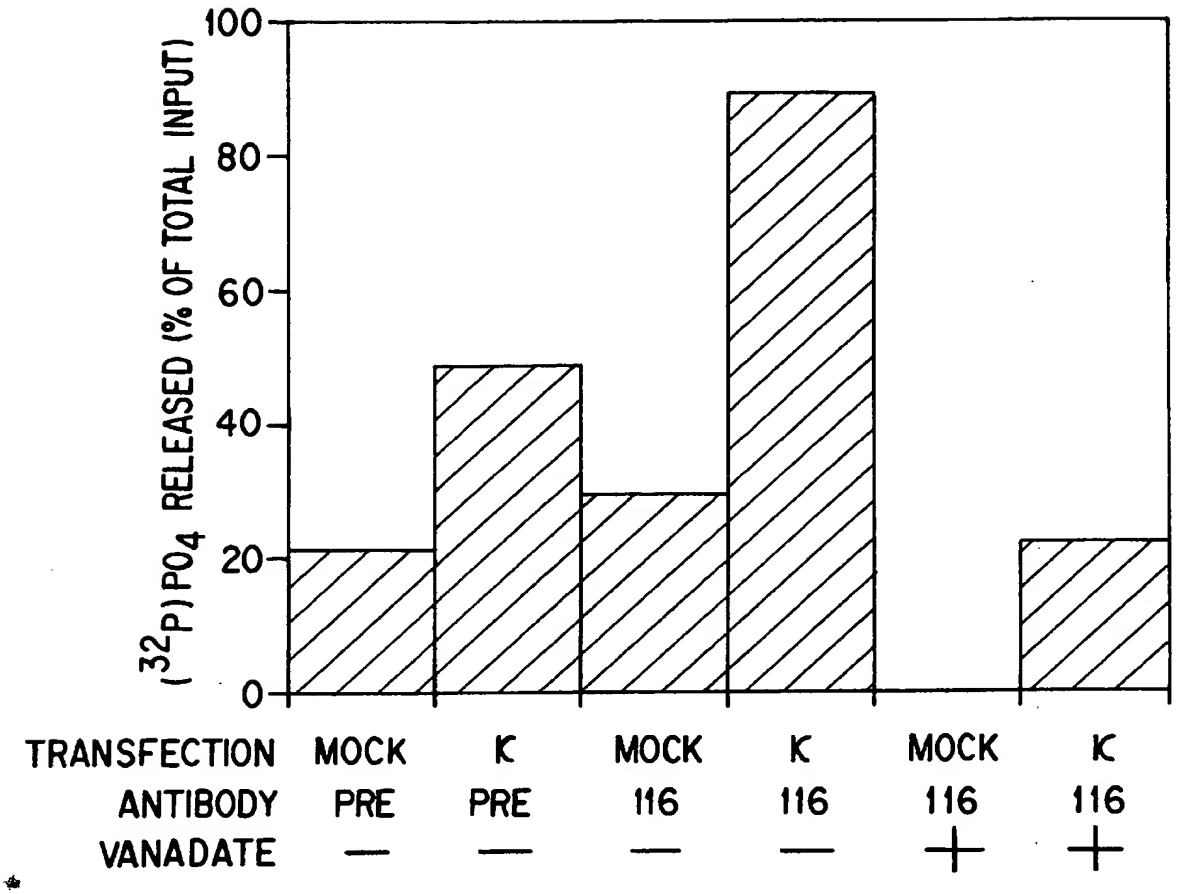

100
80
60
40
20
0
(^{32}P) PO_4 RELEASED (% OF TOTAL INPUT)
TRANSFECTION MOCK K MOCK K MOCK K
ANTIBODY PRE PRE 116 116 116 116
VANADATE — — — — + +

FIG. 8

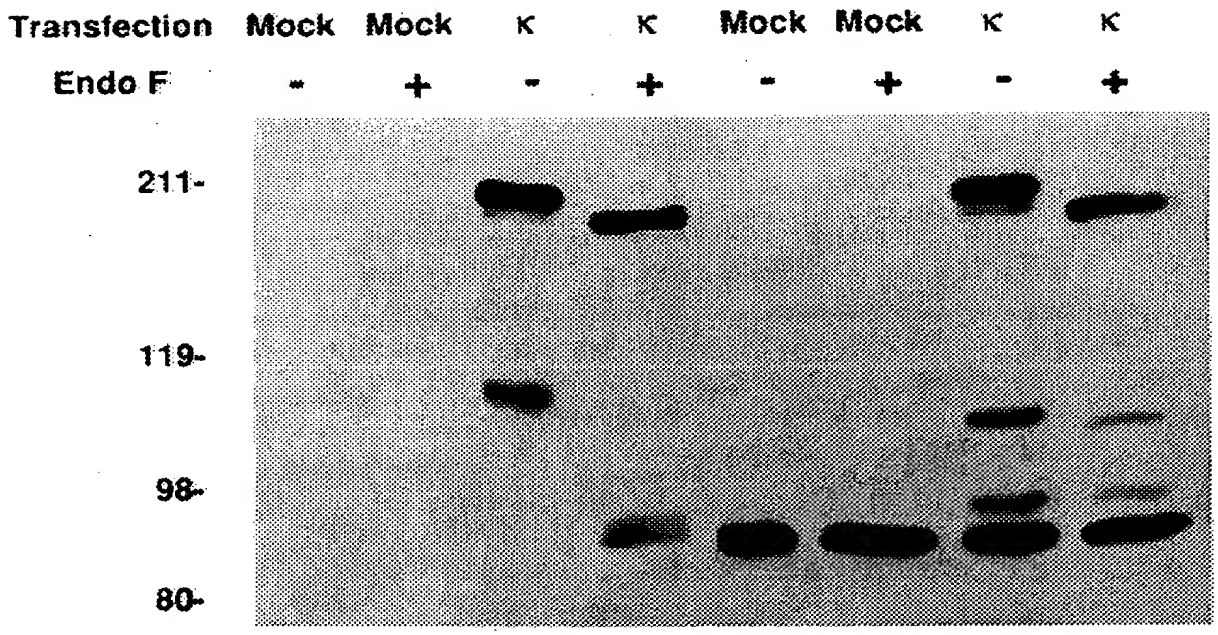


FIG. 9

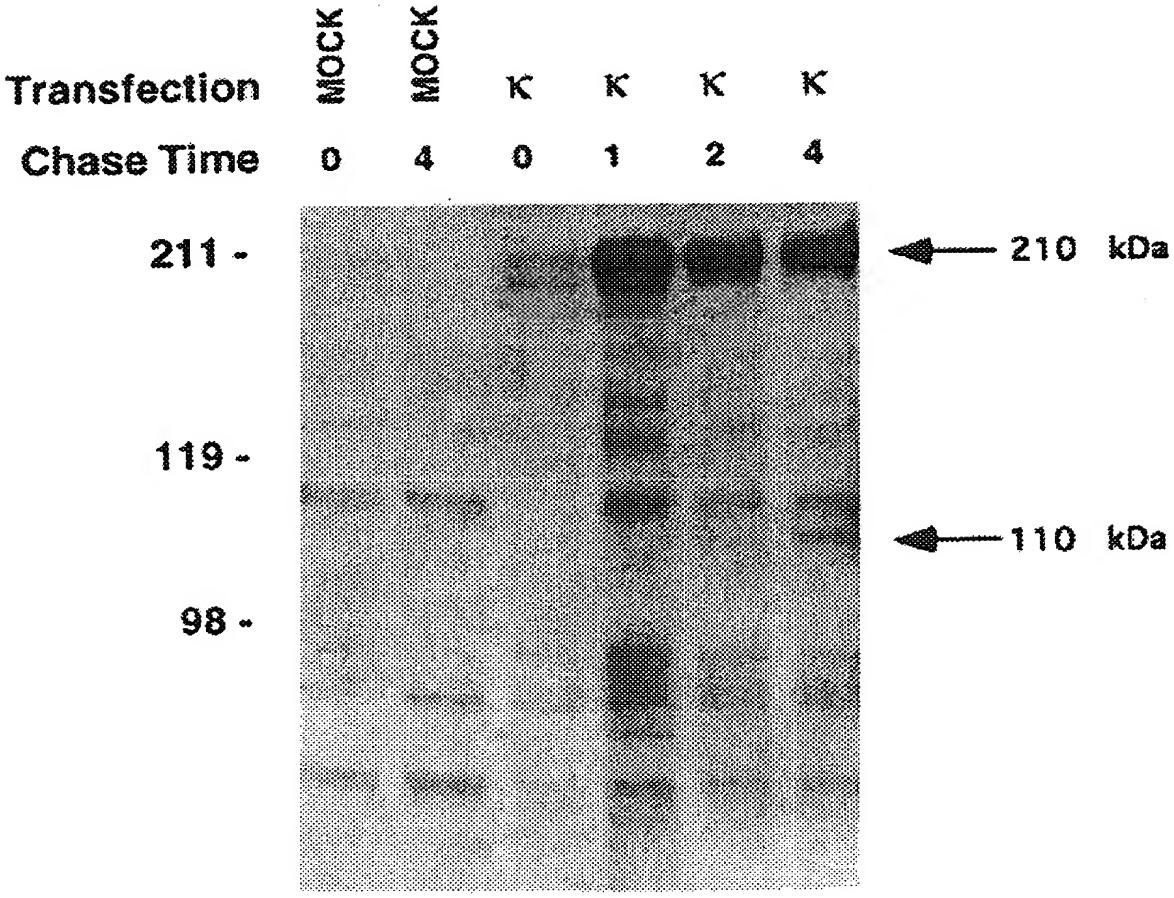

Transfection
MOCK
MOCK
K
K
K
K
Chase Time
0
4
0
1
2
4
211 -
119 -
98 -
210 kDa
110 kDa

FIG. 10

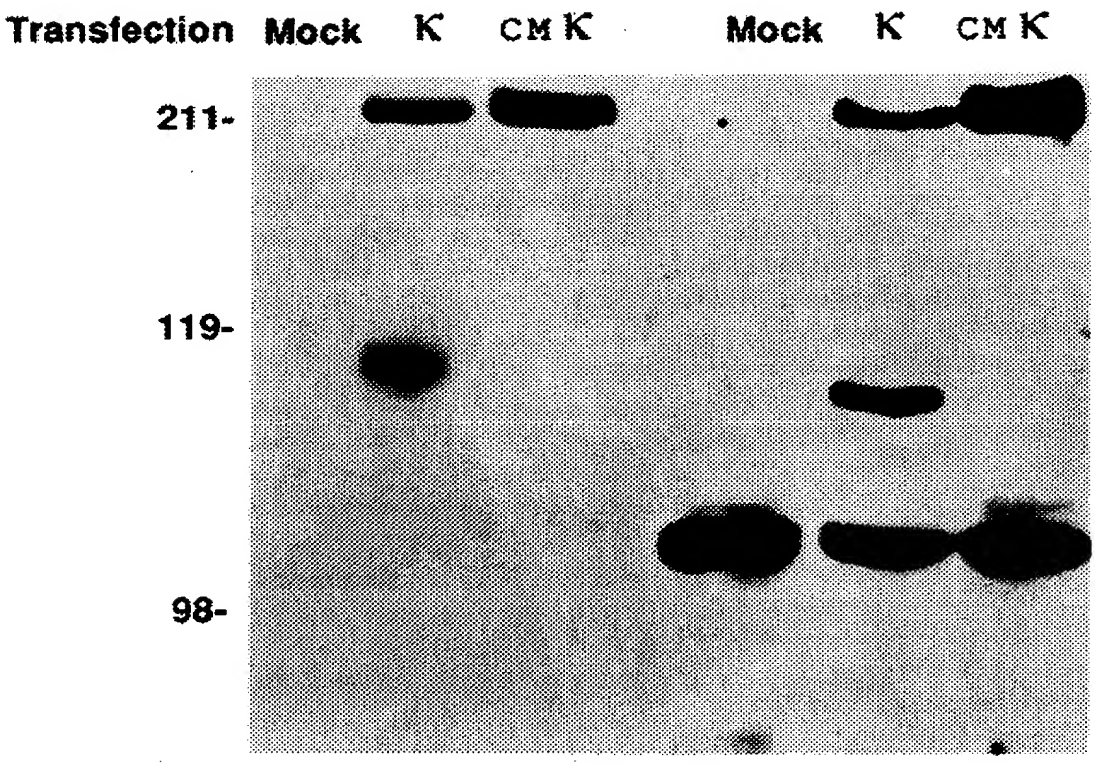


FIG. 11

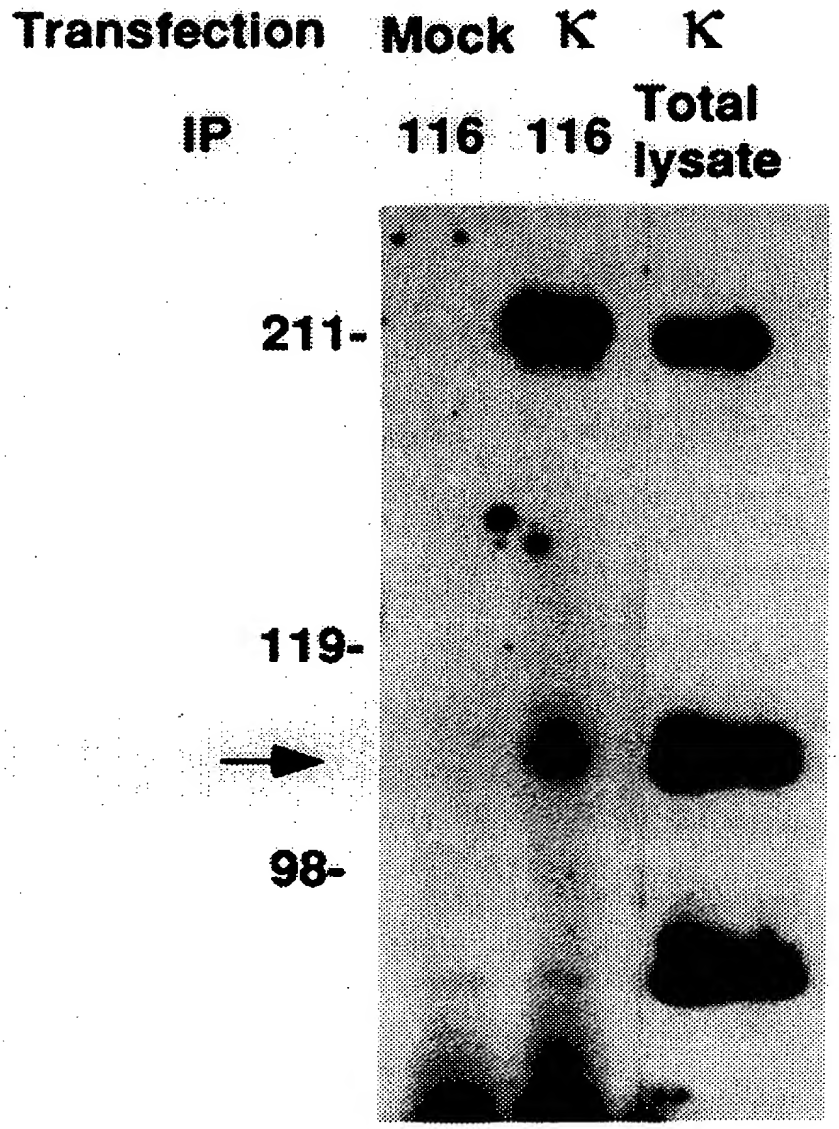


FIG. 12

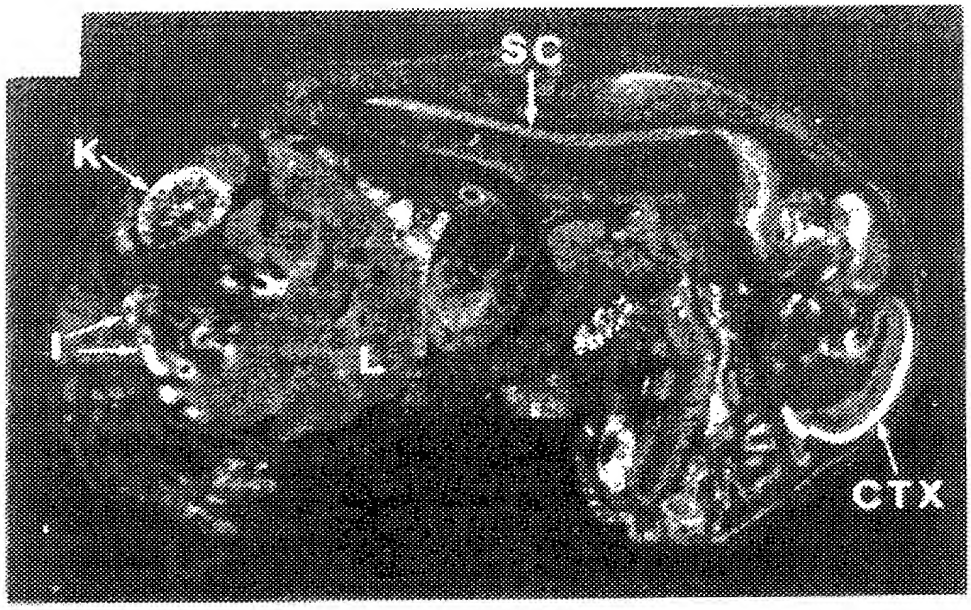


FIG. 13A

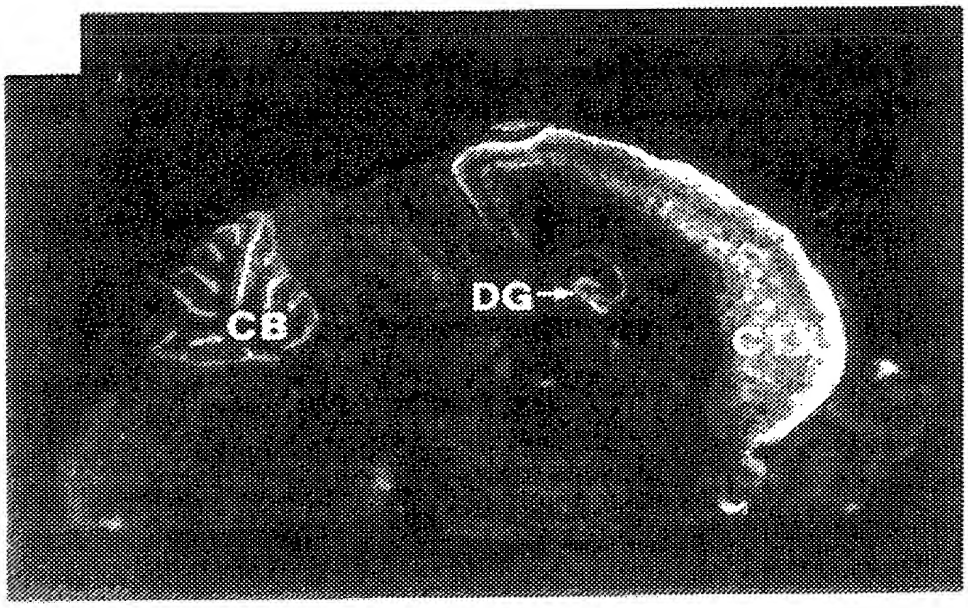


FIG. 13B

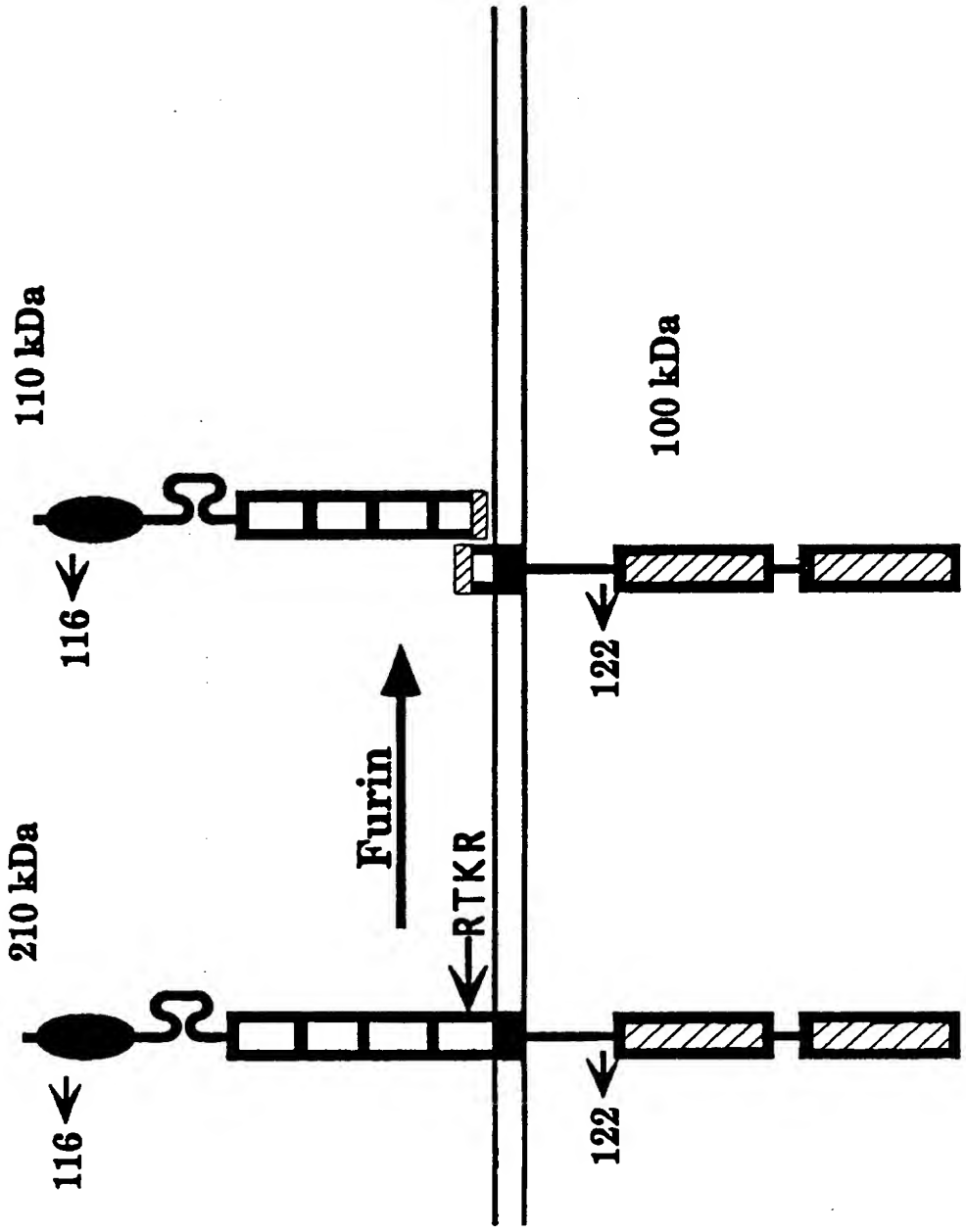


FIG. 14

```
   1 ATGGATACGACTGCGGCGGCGGCGCTGCCTGCTTTTGTGGCGCTCTTGCTCCTCTCTCCTTGGCCTCTCCTGGGATCGGC  80
   1 M  D  T  T  A  A  A  A  L  P  A  F  V  A  L  L  L  L  S  P  W  P  L  L  G  S  A  27

  81 CCAAGGCCAGTTCTCCGCAGGTGGCTGTACTTTTGATGATGGTCCAGGGGCCTGTGATTACCACCAGGATCTGTATGATG 160
  27  Q  G  Q  F  S  A  G  G  C  T  F  D  D  G  P  G  A  C  D  Y  H  Q  D  L  Y  D  D  53

 161 ACTTTGAATGGGTGCATGTTAGTGCTCAAGAGCCTCATTATCTACCACCCGAGATGCCCCAAGGTTCCTATATGATAGTG 240
  54  F  E  W  V  H  V  S  A  Q  E  P  H  Y  L  P  P  E  M  P  Q  G  S  Y  M  I  V  80

 241 GACTCTTCAGATCACGACCCTGGAGAAAAAGCCAGACTTCAGCTGCCTACAATGAAGGAGAACGACACTCACTGCATTGA 320
  81 D  S  S  D  H  D  P  G  E  K  A  R  L  Q  L  P  T  M  K  E  N  D  T  H  C  I  D  107

 321 TTTCAGTTACCTATTATATAGCCAGAAAGGACTGAATCCTGGCACTTTGAACATATTAGTTAGGGTGAATAAAGGACCTC 400
 107 F  S  Y  L  L  Y  S  Q  K  G  L  N  P  G  T  L  N  I  L  V  R  V  N  K  G  P  L  133

 401 TTGCCAATCCAATTTGGAATGTGACTGGATTCACGGGTAGAGATTGGCTTCGGGCTGAGCTAGCAGTGAGCACCTTTTGG 480
 134  A  N  P  I  W  N  V  T  G  F  T  G  R  D  W  L  R  A  E  L  A  V  S  T  F  W  160

 481 CCCAATGAATATCAGGTAATATTTGAAGCTGAAGTCTCAGGAGGGAGAAGTGGTTATATTGCCATTGATGACATCCAAGT 560
 161 P  N  E  Y  Q  V  I  F  E  A  E  V  S  G  G  R  S  G  Y  I  A  I  D  D  I  Q  V  187

 561 ACTGAGTTATCCTTGTGATAAATCTCCTCATTTCCTCCGTCTAGGGGATGTAGAGGTGAATGCAGGGCAAAACGCTACAT 640
 187  L  S  Y  P  C  D  K  S  P  H  F  L  R  L  G  D  V  E  V  N  A  G  Q  N  A  T  F  213

 641 TTCAGTGCATTGCCACAGGGAGAGATGCTGTGCATAACAAGTTATGGCTCCAGAGACGAAATGGAGAAGATATACCAGTA 720
 214  Q  C  I  A  T  G  R  D  A  V  H  N  K  L  W  L  Q  R  R  N  G  E  D  I  P  V  240

 721 GCCCAGACTAAGAACATCAATCATAGAAGGTTTGCCGCTTCCTTCAGATTGCAAGAAGTGACAAAAACTGACCAGGATTT 800
 241 A  Q  T  K  N  I  N  H  R  R  F  A  A  S  F  R  L  Q  E  V  T  K  T  D  Q  D  L  267

 801 GTATCGCTGTGTAACTCAGTCAGAACGAGGTTCCGGTGTGTCCAATTTTGCTCAACTTATTGTGAGAGAACCGCCAAGAC 880
 267  Y  R  C  V  T  Q  S  E  R  G  S  G  V  S  N  F  A  Q  L  I  V  R  E  P  P  R  P  293

 881 CCATTGCTCCTCCTCAGCTTCTTGGTGTTGGGCCTACATATTTGCTGATCCAACTAAATGCCAACTCGATCATTGGCGAT 960
 294  I  A  P  P  Q  L  L  G  V  G  P  T  Y  L  L  I  Q  L  N  A  N  S  I  I  G  D  320

 961 GGTCCTATCATCCTGAAAGAAGTAGAGTACCGAATGACATCAGGATCCTGGACAGAAACCCATGCAGTCAATGCTCCAAC 1040
 321 G  P  I  I  L  K  E  V  E  Y  R  M  T  S  G  S  W  T  E  T  H  A  V  N  A  P  T  347
```

FIG.15A

```
1041  TTACAAATTATGGCATTTAGATCCAGATACCGAATATGAGATCCGAGTTCTACTTACAAGACCTGGTGAAGGTGGAACGG  1120
 347   Y  K  L  W  H  L  D  P  D  T  E  Y  E  I  R  V  L  L  T  R  P  G  E  G  G  T  G   373

1121  GGCTCCCAGGACCTCCACTAATCACCAGAACAAAATGTGCAGAACCTATGAGAACCCCAAAGACATTAAAGATTGCTGAA  1200
 374   L  P  G  P  P  L  I  T  R  T  K  C  A  E  P  M  R  T  P  K  T  L  K  I  A  E    400

1201  ATACAGGCAAGACGGATTGCTGTGGACTGGGAATCCTTGGGTTACAACATTACGCGTTGCCACACTTTTAATGTCACTAT  1280
 401   I  Q  A  R  R  I  A  V  D  W  E  S  L  G  Y  N  I  T  R  C  H  T  F  N  V  T  I   427

1281  CTGCTACCATTACTTCCGTGGTCACAACGAGAGCAAGGCAGACTGTTTGGACATGGACCCCAAAGCCCCTCAGCATGTTG  1360
 427   C  Y  H  Y  F  R  G  H  N  E  S  K  A  D  C  L  D  M  D  P  K  A  P  Q  H  V  V   453

1361  TGAACCATCTGCCACCTTATACAAATGTCAGCCTCAAGATGATCCTAACCAATCCAGAGGGAAGGAAGGAGAGTGAAGAG  1440
 454   N  H  L  P  P  Y  T  N  V  S  L  K  M  I  L  T  N  P  E  G  R  K  E  S  E  E    480

1441  ACAATTATTCAAACTGATGAAGATGTGCCTGGTCCCGTACCAGTAAAATCTCTTCAAGGAACATCCTTTGAAAATAAGAT  1520
 481   T  I  I  Q  T  D  E  D  V  P  G  P  V  P  V  K  S  L  Q  G  T  S  F  E  N  K  I   507

1521  CTTCTTGAACTGGAAAGAACCTTTGGATCCAAATGGAATCATCACTCAATATGAGATCAGCTATAGCAGTATAAGATCAT  1600
 507   F  L  N  W  K  E  P  L  D  P  N  G  I  I  T  Q  Y  E  I  S  Y  S  S  I  R  S  F   533

1601  TTGATCCTGCAGTCCCAGTGGCTGGACCTCCCCAGACTGTATCAAATTTATGGAACAGTACACACCATGTCTTTATGCAT  1680
 534   D  P  A  V  P  V  A  G  P  P  Q  T  V  S  N  L  W  N  S  T  H  H  V  F  M  H    560

1681  CTCCACCCTGGAACCACGTACCAGTTTTTCATAAGAGCCAGCACGGTCAAAGGCTTTGGTCCAGCCACAGCCATCAATGT  1760
 561   L  H  P  G  T  T  Y  Q  F  F  I  R  A  S  T  V  K  G  F  G  P  A  T  A  I  N  V   567

1761  CACCACCAATATCTCAGCTCCAACTTTACCTGACTATGAAGGAGTTGATGCCTCTCTCAATGAAACTGCCACCACAATAA  1840
 587   T  T  N  I  S  A  P  T  L  P  D  Y  E  G  V  D  A  S  L  N  E  T  A  T  T  I  T   613

1841  CTGTATTGTTGAGACCAGCACAAGCCAAAGGTGCTCCTATCAGTGCTTATCAGATTGTTGTGGAAGAACTGCACCCACAC  1920
 614   V  L  L  R  P  A  Q  A  K  G  A  P  I  S  A  Y  Q  I  V  V  E  E  L  H  P  H    640

1921  CGAACCAAGAGAGAAGCCGGAGCCATGGAATGCTACCAGGTTCCTGTCACATACCAAAATGCCATGAGTGGGGGTGCACC  2000
 641   R  T  K  R  E  A  G  A  M  E  C  Y  Q  V  P  V  T  Y  Q  N  A  M  S  G  G  A  P   667

2001  GTATTACTTTGCTGCAGAACTACCCCCGGGAAACCTACCTGAGCCTGCCCCGTTCACTGTGGGTGACAATCGGACCTACC  2080
 667   Y  Y  F  A  A  E  L  P  P  G  N  L  P  E  P  A  P  F  T  V  G  D  N  R  T  Y  Q   693

2081  AAGGCTTTTGGAACCCTCCTTTGGCTCCGCGCAAAGGATACAACATCTATTTCCAGGCGATGAGCAGTGTGGAGAAGGAA  2160
 694   G  F  W  N  P  P  L  A  P  R  K  G  Y  N  I  Y  F  Q  A  M  S  S  V  E  K  E    720
```

FIG.15B

```
2161  ACTAAAACCCAGTGCGTACGCATTGCTACAAAAGCAGCAACAGAAGAACCAGAAGTGATCCCAGATCCCGCCAAGCAGAC  2240
 721  T  K  T  Q  C  V  R  I  A  T  K  A  A  T  E  E  P  E  V  I  P  D  P  A  K  Q  T   747

2241  AGACAGAGTGGTGAAAATAGCAGGAATTAGTGCTGGAATTTTGGTGTTCATCCTCCTTCTCCTAGTTGTCATATTAATTG  2320
 747  D  R  V  V  K  I  A  G  I  S  A  G  I  L  V  F  I  L  L  L  L  V  V  I  L  I  V   773

2321  TAAAAAAGAGCAAACTTGCTAAAAAACGCAAAGATGCCATGGGGAATACCCGGCAGGAGATGACTCACATGGTGAATGCA  2400
 774  K  K  S  K  L  A  K  K  R  K  D  A  M  G  N  T  R  Q  E  M  T  H  M  V  N  A   800

2401  ATGGATCGAAGTTATGCTGATCAGAGCACTCTGCATGCAGAAGATCCTCTTTCCATCACCTTCATGGACCAACATAACTT  2480
 801  M  D  R  S  Y  A  D  Q  S  T  L  H  A  E  D  P  L  S  I  T  F  M  D  Q  H  N  F   827

2481  TAGTCCAAGATATGAGAACCACAGTGCTACAGCAGAGTCCAGTCGCCTTCTAGACGTACCTCGCTACCTCTGTGAGGGGA  2560
 827  S  P  R  Y  E  N  H  S  A  T  A  E  S  S  R  L  L  D  V  P  R  Y  L  C  E  G  T   853

2561  CGGAATCCCCTTACCAGACAGGACAGCTGCATCCAGCCATCAGGGTAGCTGATTTACTGCAGCACATTAATCTCATGAAG  2640
 854  E  S  P  Y  Q  T  G  Q  L  H  P  A  I  R  V  A  D  L  L  Q  H  I  N  L  M  K   880

2641  ACATCAGACAGCTATGGGTTCAAAGAGGAATATGAGAGCTTTTTTGAAGGACAGTCAGCATCTTGGGATGTAGCTAAAAA  2720
 881  T  S  D  S  Y  G  F  K  E  E  Y  E  S  F  F  E  G  Q  S  A  S  W  D  V  A  K  K   907

2721  AGATCAAAATAGAGCAAAAAACCGATATGGAAACATTATAGCATATGATCACTCCAGAGTGATTTTGCAACCCGTAGAGG  2800
 907  D  Q  N  R  A  K  N  R  Y  G  N  I  I  A  Y  D  H  S  R  V  I  L  Q  P  V  E  D   933

2801  ATGATCCTTCCTCAGATTATATTAATGCCAACTATATTGATGGCTACCAGAGACCAAGTCATTACATTGCAACCCAAGGT  2880
 934  D  P  S  S  D  Y  I  N  A  N  Y  I  D  G  Y  Q  R  P  S  H  Y  I  A  T  Q  G   960

2881  CCCGTTCATGAAACAGTGTATGATTTCTGGAGGATGATTTGGCAAGAACAATCTGCTTGCATTGTGATGGTTACAAATTT  2960
 961  P  V  H  E  T  V  Y  D  F  W  R  M  I  W  Q  E  Q  S  A  C  I  V  M  V  T  N  L   987

2961  AGTTGAGGTTGGCCGGGTTAAATGCTATAAATATTGGCCTGATGATACTGAAGTTTATGGTGACTTCAAAGTAACGTGTG  3040
 987  V  E  V  G  R  V  K  C  Y  K  Y  W  P  D  D  T  E  V  Y  G  D  F  K  V  T  C  V  1013

3041  TAGAAATGGAACCACTTGCTGAATATGTAGTTAGGACATTCACCCTGGAAAGGAGGGGGTACAATGAAATCCGTGAAGTT  3120
1014  E  M  E  P  L  A  E  Y  V  V  R  T  F  T  L  E  R  R  G  Y  N  E  I  R  E  V   1040

3121  AAACAGTTCCATTTCACGGGCTGGCCTGACCATGGAGTGCCCTACCATGCTACAGGGCTGCTTTCCTTTATCCGGCGAGT  3200
1041  K  Q  F  H  F  T  G  W  P  D  H  G  V  P  Y  H  A  T  G  L  L  S  F  I  R  R  V  1067
```

FIG.15C

```
3201  CAAGTTATCAAACCCTCCCAGTGCTGGCCCCATCGTTGTACATTGCAGTGCTGGTGCTGGACGAACTGGCTGCTACATTG  3280
1067   K  L  S  N  P  P  S  A  G  P  I  V  V  H  C  S  A  G  A  G  R  T  G  C  Y  I  V  1093

3281  TGATTGACATCATGCTAGACATGGCTGAAAGAGAGGGTGTTGTTGATATTTACAATTGTGTCAAAGCCTTAAGATCTCGG  3360
1094    I  D  I  M  L  D  M  A  E  R  E  G  V  V  D  I  Y  N  C  V  K  A  L  R  S  R   1120

3361  CGTATTAATATGGTCCAGACAGAGGAACAGTACATTTTTATTCATGATGCCATTTTAGAAGCCTGCTTATGTGGAGAAAC  3440
1121  R  I  N  M  V  Q  T  E  E  Q  Y  I  F  I  H  D  A  I  L  E  A  C  L  C  G  E  T  1147

3441  TGCCATACCTGTCTGTGAATTTAAAGCTGCATATTTTGATATGATTAGAATAGACTCCCAGACTAACTCTTCACATCTCA  3520
1147   A  I  F  V  C  E  F  K  A  A  Y  F  D  M  I  R  I  D  S  Q  T  N  S  S  H  L  K  1173

3521  AGGATGAATTTCAGACTCTGAATTCAGTCACCCCTCGACTACAAGCTGAAGACTGCAGTATAGCGTGCCTGCCAAGGAAC  3600
1174    D  E  F  Q  T  L  N  S  V  T  P  R  L  Q  A  E  D  C  S  I  A  C  L  P  R  N   1200

3601  CATGACAAGAACCGTTTCATGGACATGCTGCCACCTGACAGATGTCTGCCTTTTTTAATTACAATTGATGGGGAGAGCAG  3680
1201  H  D  K  N  R  F  M  D  M  L  P  P  D  R  C  L  P  F  L  I  T  I  D  G  E  S  S  1227

3681  TAACTACATCAATGCTGCTCTTATGGACAGCTACAGGCAACCAGCTGCTTTCATCGTCACACAATACCCTCTGCCAAACA  3760
1227   N  Y  I  N  A  A  L  M  D  S  Y  R  Q  P  A  A  F  I  V  T  Q  Y  P  L  P  N  T  1253

3761  CTGTAAAAGACTTCTGGAGATTAGTGTATGATTATGGCTGTACCTCCATTGTGATGTTAAACGAAGTCGACTTGTCCCAG  3840
1254    V  K  D  F  W  R  L  V  Y  D  Y  G  C  T  S  I  V  M  L  N  E  V  D  L  S  Q   1280

3841  GGCTGCCCTCAGTACTGGCCAGAGGAAGGGATGCTACGATATGGCCCCATCCAAGTGGAATGTATGTCTTGTTCAATGGA  3920
1281  G  C  P  Q  Y  W  P  E  E  G  M  L  R  Y  G  P  I  Q  V  E  C  M  S  C  S  M  D  1307

3921  CTGTGATGTGATCAACCGGATTTTTAGGATATGCAATCTAACAAGACCACAGGAAGGTTATCTGATGGTGCAACAGTTTC  4000
1307   C  D  V  I  N  R  I  F  R  I  C  N  L  T  R  P  Q  E  G  Y  L  M  V  Q  Q  F  Q  1333

4001  AGTACCTAGGATGGGCTTCTCATCGAGAAGTGCCTGGATCCAAAAGGTCATTCTTGAAACTGATACTTCAGGTGGAAAAG  4080
1334    Y  L  G  W  A  S  H  R  E  V  P  G  S  K  R  S  F  L  K  L  I  L  Q  V  E  K   1360

4081  TGGCAGGAGGAATGCGAGGAAGGGGAAGGCCGGACGATTATCCACTGCCTAAATGGTGGCGGGCGAAGTGGCATGTTCTG  4160
1361  W  Q  E  E  C  E  E  G  E  G  R  T  I  I  H  C  L  N  G  G  G  R  S  G  M  F  C  1387

4161  TGCTATAGGCATCGTTGTTGAAATGGTGAAACGGCAAAATGTTGTCGATGTTTTCCATGCAGTAAAGACACTGAGGAACA  4240
1387   A  I  G  I  V  V  E  M  V  K  R  Q  N  V  V  D  V  F  H  A  V  K  T  L  R  N  S  1413
```

FIG.15D

4241 GCAAGCCAAACATGGTGGAAGCCCCCGGAGCAATACCGTTTCTGCTATGATGTAGCTTTGGAGTACCTGGAATCATCTTAG 4320
1414 K P N M V E A P E Q Y R F C Y D V A L E Y L E S S * 1439
SEQ. ID NO: 2
4321 TTGGGTGAGACTCTTTAAAGTGCATCCATGAAGAAACCTGTCCATCTATTGAGCCAGCAGCTGTTGTACCTGTTACACTT 4400
4401 GTGCAGAAAGATTTTAATGTGGGGGGTGGGAGACTTTTACATTTGAGAGGTAAAAGTATTTTTTTTATGAAGTTGTGTAT 4480
4481 CTTAATAAAAAGAACTGAATTAGTTTTTATTACTATATTAAAGCATCAACATTTCATGCCACATAAAATTATATTTAATA 4560
4561 AGAACCAGATTGAAATGAGAACGTATTGGTGTTTGTACAGTGAACATGCCACCTTTTTCCATGGTTTCAGGTAGTGCAGC 4640
4641 TACCACATGTT 4651
SEQ. ID NO: 4

FIG.15E

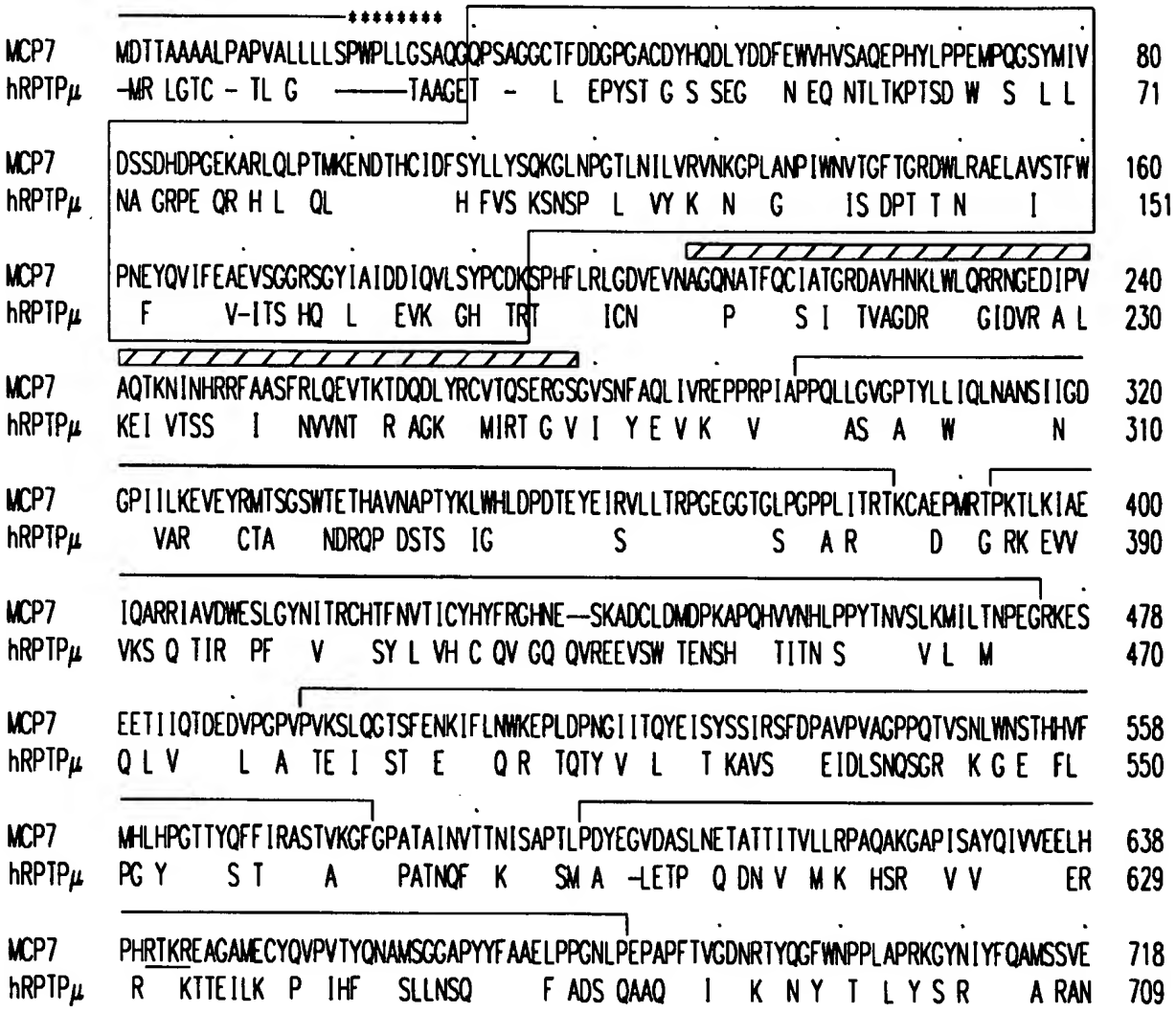


FIG.16A

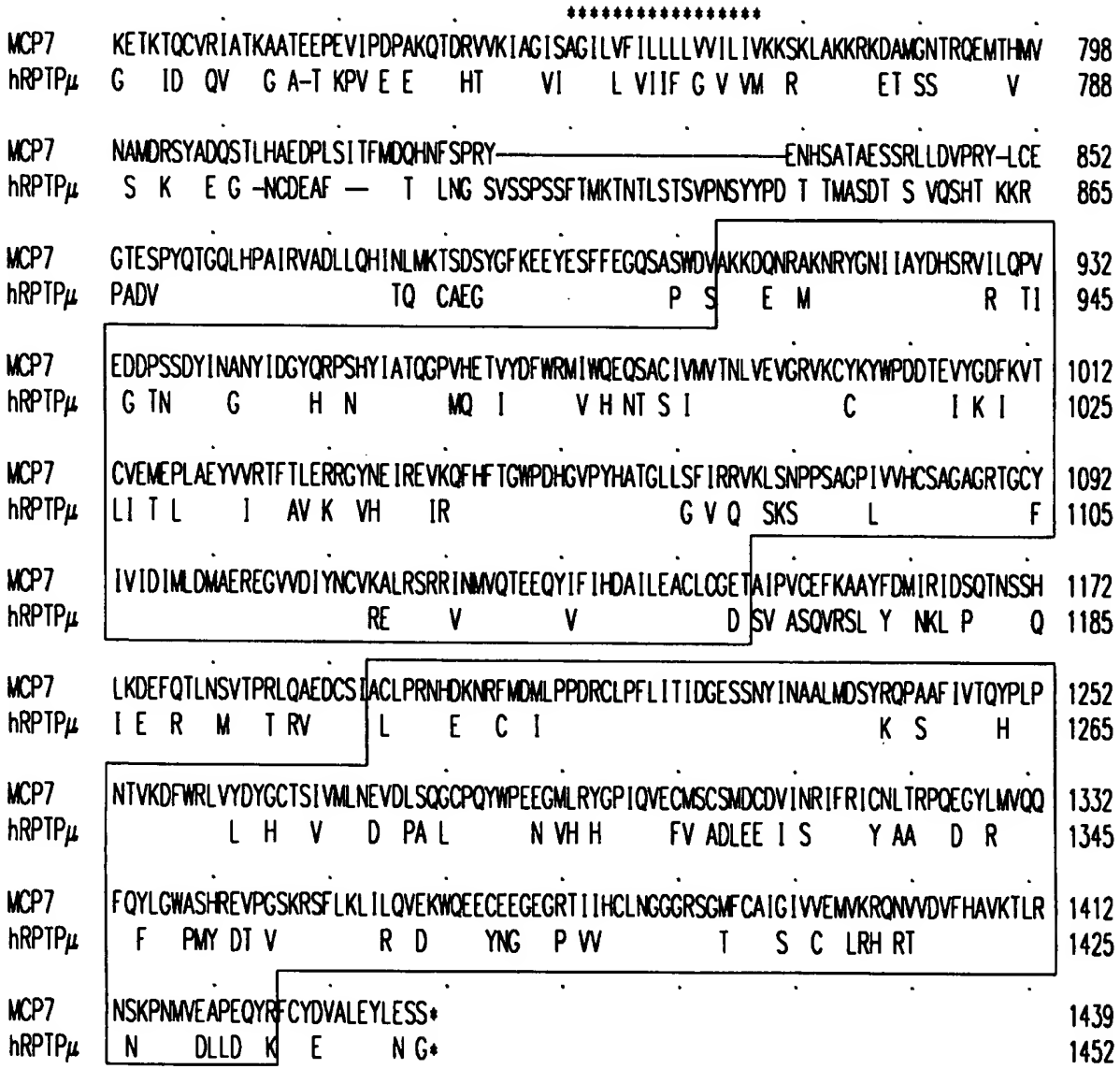


FIG.16B

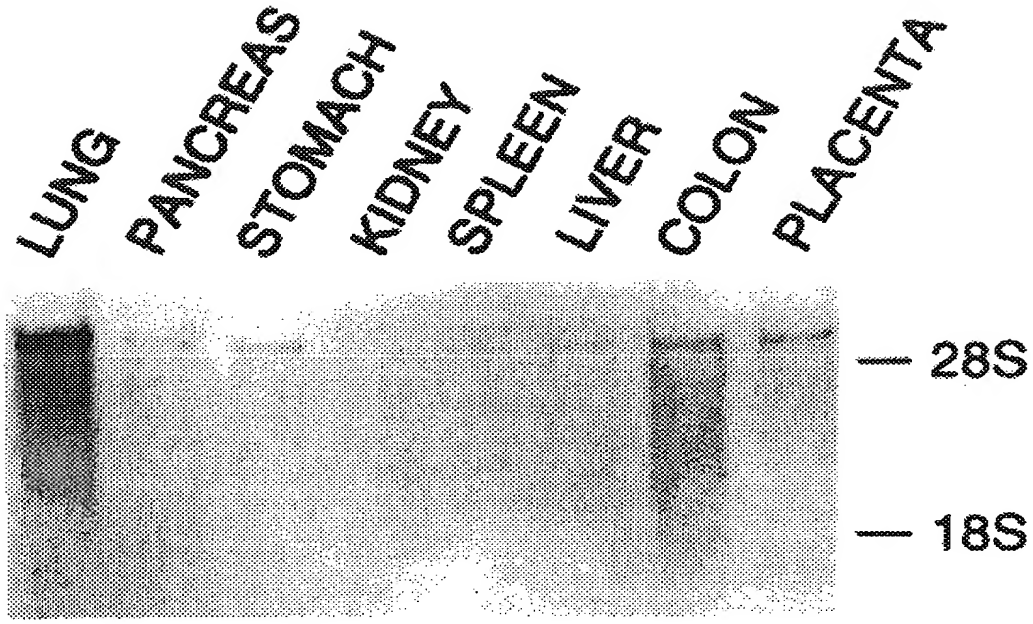

LUNG
PANCREAS
STOMACH
KIDNEY
SPLEEN
LIVER
COLON
PLACENTA
28S
18S

FIG. 17

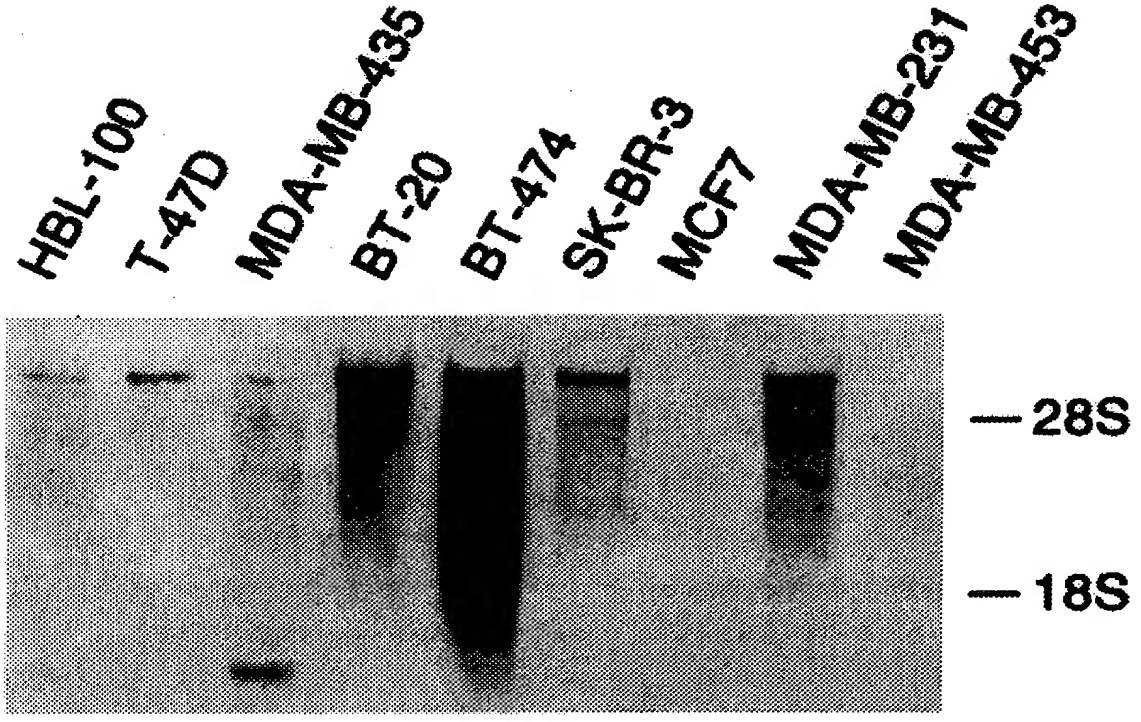

HBL-100
T-47D
MDA-MB-435
BT-20
BT-474
SK-BR-3
MCF7
MDA-MB-231
MDA-MB-453
28S
18S

FIG. 18

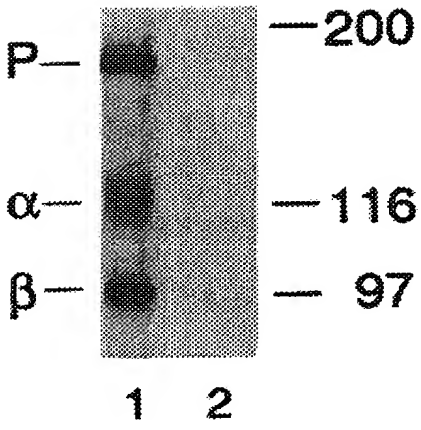


FIG. 19A

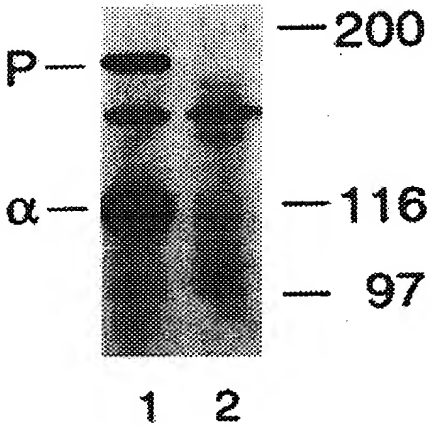


FIG. 19B

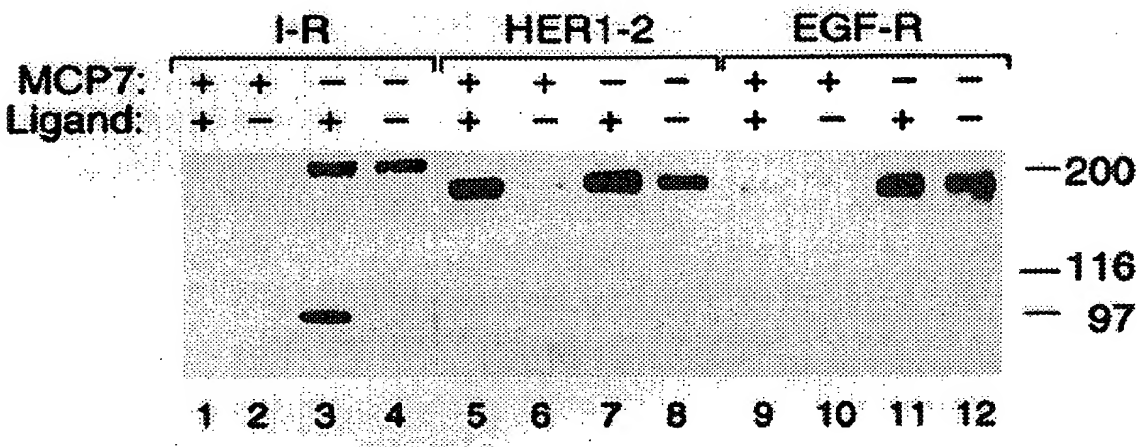


FIG. 20A

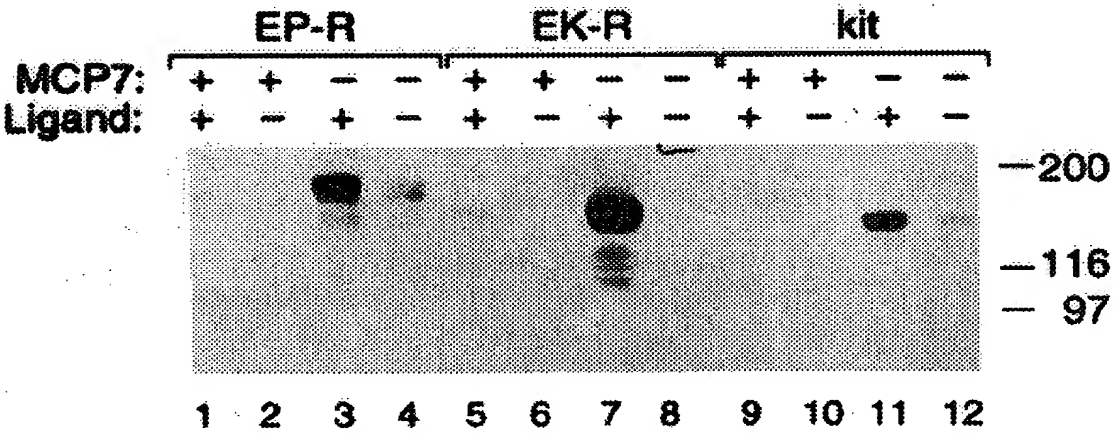


FIG. 20B

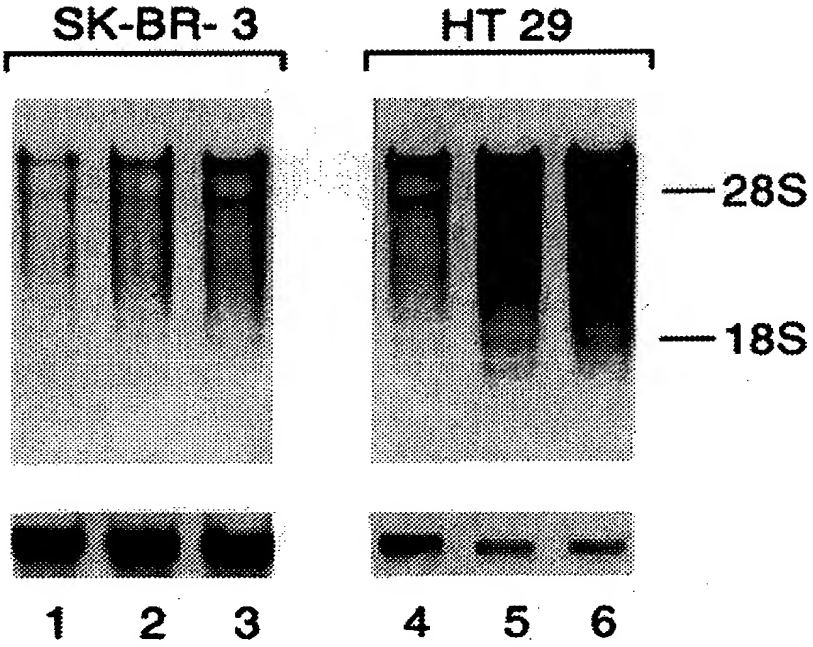


FIG. 21A FIG. 21B

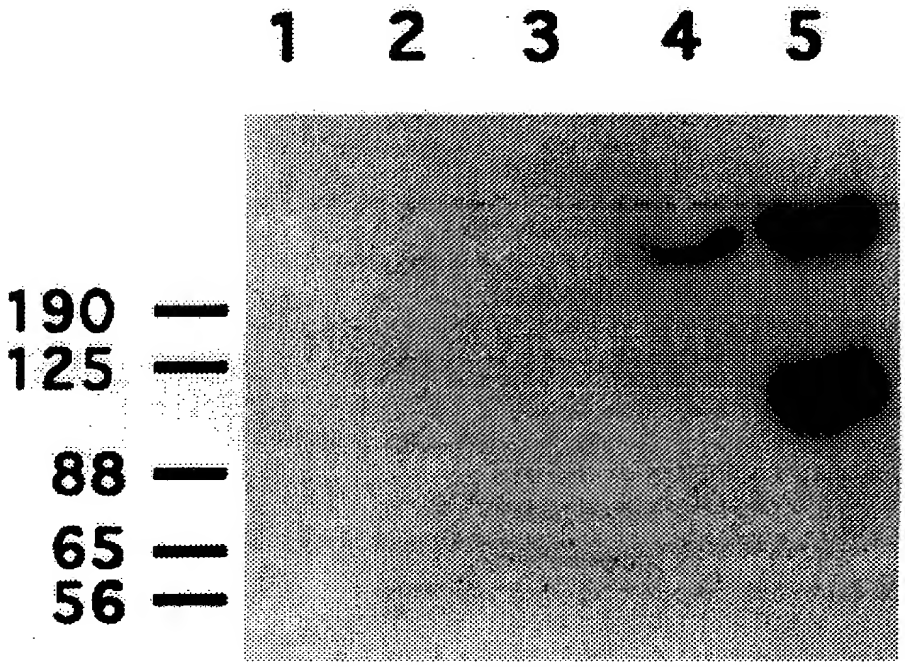


FIG. 22A

CONTROL

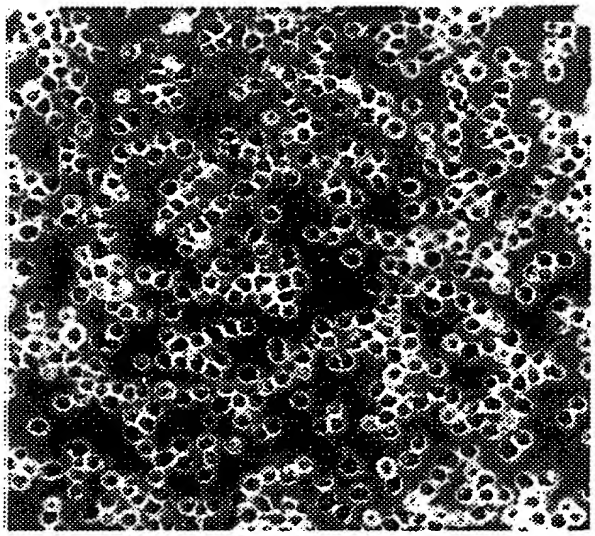


FIG. 22B

R-PTP-K

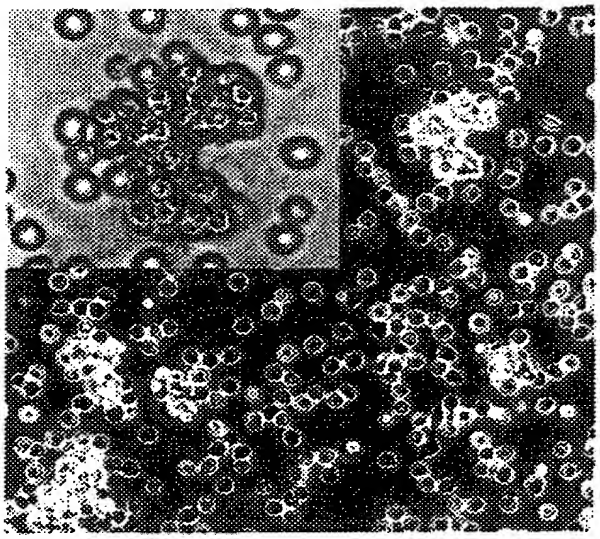


FIG. 22C

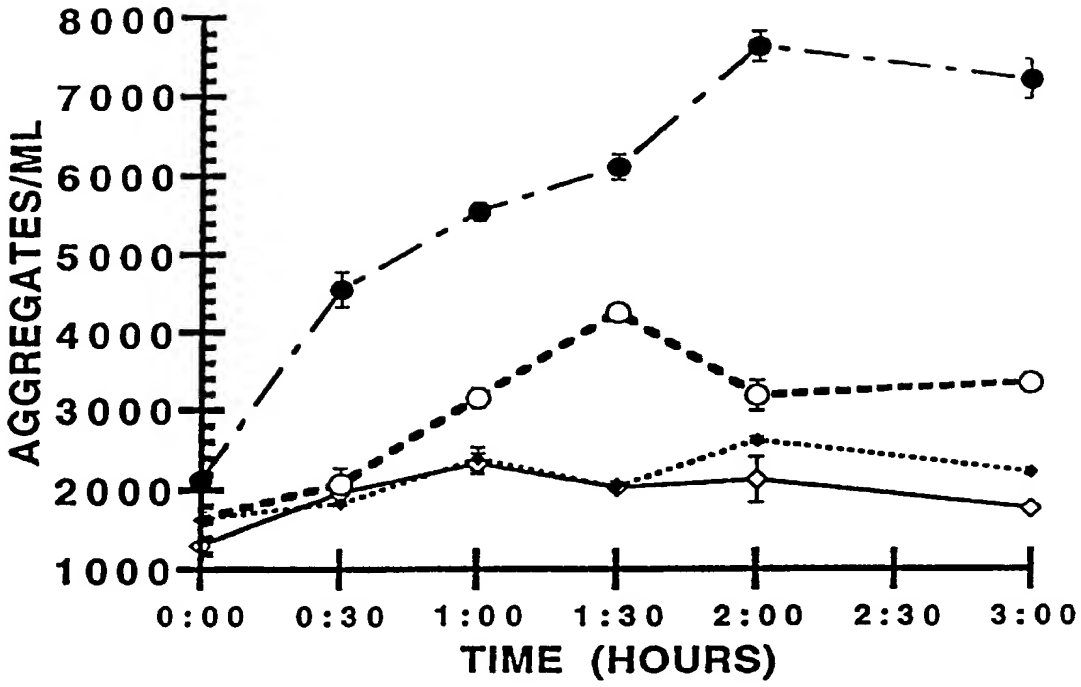


FIG. 22D

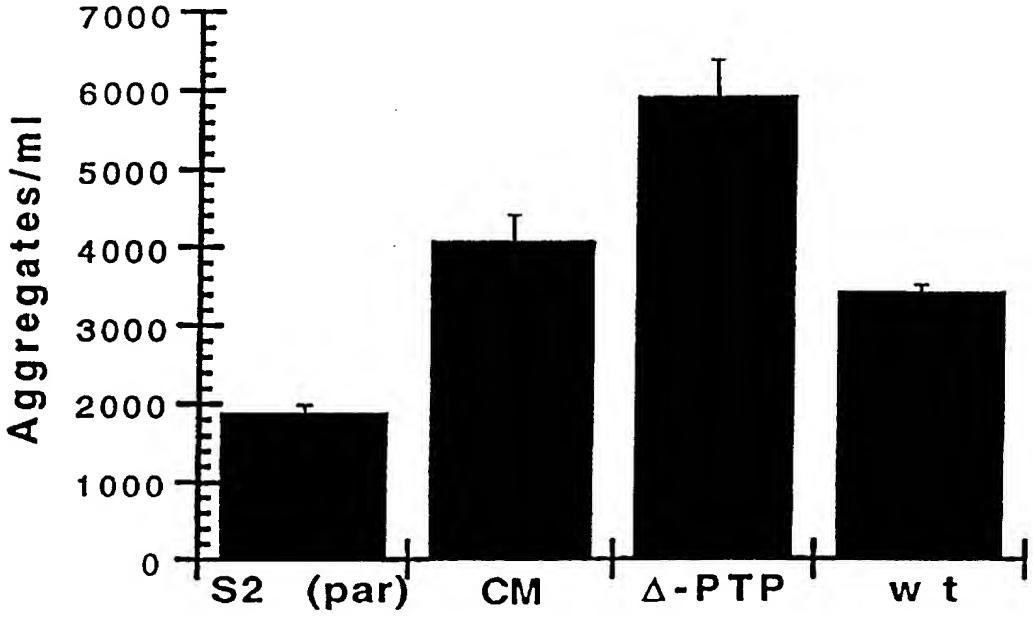


FIG. 22E

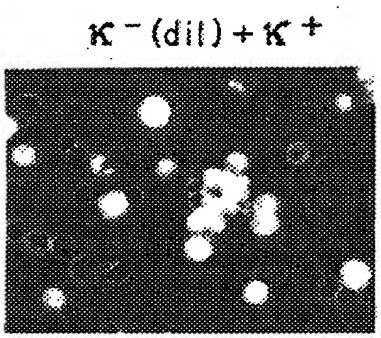


FIG. 23A

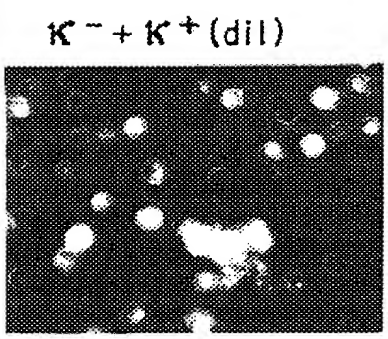


FIG. 23B

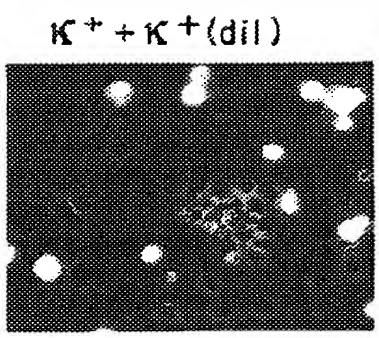
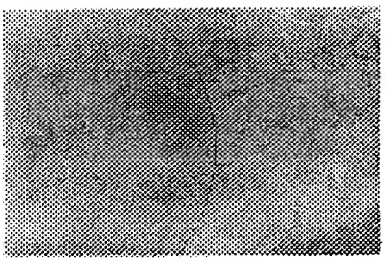


FIG. 23C

FIG. 24A



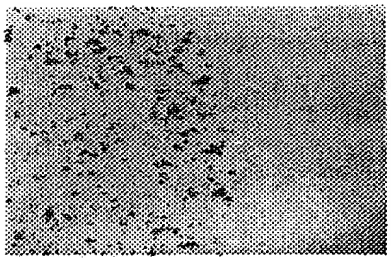
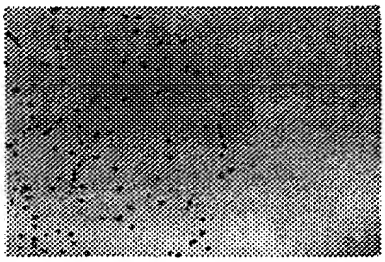


FIG. 24B

FIG. 24C



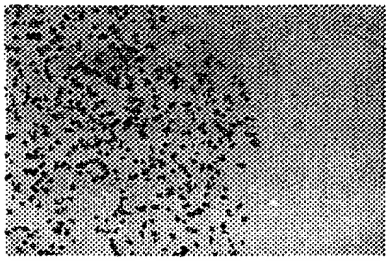


FIG. 24D